

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 12:33:12 ; Search time 181 Seconds
(without alignments)
1788.500 Million cell updates/sec

Title: US-09-634-287E-2

Perfect score: 4570
Sequence: 1 MSQTSHPGRGLAGRWLNGA.....LHRRQAILEILRRRPWAGRK 837

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4570	100.0	837	2 AAW75425	Aaw75425 Human agg
2	4570	100.0	837	7 ADJ69542	Adj69542 Human hea
3	4570	100.0	837	8 ADS20209	Ads20209 Human agg
4	4567	99.9	846	8 ADS20232	Ads20232 Human agg
5	4566	99.9	837	4 AAG78228	Aag78228 Human agg
6	4566	99.9	837	7 ADB85488	Adb85488 Human agg
7	4566	99.8	840	3 AAB21256	Aab21256 Human met
8	4563	99.8	837	3 AAY99429	Aay99429 Human PRO
9	4563	99.8	837	4 AAB66178	Aab66178 Protein o
10	4563	99.8	837	4 AAU29199	Aau29199 Human PRO
11	4563	99.8	837	6 ABUS8575	Abus8575 Human PRO
12	4563	99.8	837	6 ABUS8123	Abus8123 Novel hum
13	4563	99.8	837	6 ABUS4438	Abus4438 Human sec
14	4563	99.8	837	6 ABR66312	Abr66312 Human sec
15	4563	99.8	837	6 ABR65702	Abr65702 Human sec
16	4563	99.8	837	6 ABUS9642	Abus9642 Human sec
17	4563	99.8	837	6 ABUS2881	Abus2881 Human PRO
18	4563	99.8	837	6 ABUS9002	Abus9002 Novel hum
19	4563	99.8	837	6 ABR68251	Abr68251 Human sec
20	4563	99.8	837	6 ABR96304	Abr96304 Novel hum
21	4563	99.8	837	6 ABUS2735	Abus2735 Human sec
22	4563	99.8	837	6 ABO08812	Abo08812 Human sec
23	4563	99.8	837	6 ABO02864	Abo02864 Human sec
24	4563	99.8	837	6 ABR75018	Abr75018 Human sec
25	4563	99.8	837	6 ABR94780	Abr94780 Human sec

ALIGNMENTS

RESULT 1
AAW75425
ID AAW75425 standard; protein; 837 AA.
XX AC AAW75425;
XX DT 30-MAR-1999 (first entry)
XX DE Human aggrecan degrading metalloprotease 1.
XX KW Human; aggrecan degrading metalloprotease; cartilage; proteoglycan;
KW interglobular domain; matrix metalloprotease; bovine; interleukin-1beta;
KW primer; PCR; amplification; inhibitor; cleavage; inhibitor; ADMP;
KW arthritis; joint injury; pseudogout.
XX OS Homo sapiens.
XX PN WO9905291-A2.
XX PD 04-FEB-1999.
XX PP 24-JUL-1998; 98WO-US015438.
XX PR 25-JUL-1997; 97US-0053850P.
PR 15-AUG-1997; 97US-0055836P.
PR 16-OCT-1997; 97US-0062169P.
PA (DUPO) DU PONT PHARM CO.
PI Arner EC, Burn TC, Copeland RA, Decicco CP, Liu R, Magolda R;
PI Pratta M, Solomon KA, Tortorella MD, Trzaskos JW, Yang F;
XX WPI: 1999-142943/12.
DR N-PSDB; AAX00725.

New isolated aggrecan degrading metallo proteases - used to develop products for treating, e.g. osteoarthritis, joint injury, reactive arthritis, psoriatic arthritis or juvenile rheumatoid arthritis.

Claim 25; Page 61-62; 73pp; English.

This sequence represents the human aggrecan degrading metalloprotease 1 (ADMP-1). ADMP-1 and ADMP-2 (AAW75426) are novel proteases that cleave the aggrecan (a major cartilage proteoglycan) between residues Glu373-Ala374 of the interglobular domain (compared with cleavage between Asn341-Phe342 by the matrix metalloproteases MMP-1, -2, -3, -7, -8, -9 and -13). ADMP-1 and ADMP-2 were isolated and purified from the conditioned media of bovine nasal cartilage stimulated by interleukin-1beta. The

CC purified proteins were partially sequenced and primers were synthesised
 CC based on the resultant amino acid sequences (AA00727-X00732 for ADMP-1
 CC and AA00733-X00736 for ADMP-2). These were used to isolate the
 CC corresponding genes from cDNA. The ADMP polypeptides can be used for
 CC identifying inhibitors of ADMP activity which would prevent cleavage of
 CC the aggrecan core protein, thereby decreasing the loss of aggrecan from
 CC cartilage. Such inhibitors can be used for treating diseases such as
 CC osteoarthritis, joint injury, reactive arthritis, acute pyrophosphate
 CC arthritis (pseudogout), psoriatic arthritis and juvenile rheumatoid
 CC arthritis
 XX
 SQ Sequence 837 AA;

Query Match 100.0%; Score 4570; DB 2; Length 837;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 837; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQTGSHPGRLAGRWLWGAQPCLLPIVPLSLWMLLLLLLLASLLPSARLASPLPREE 60
 DB 1 MSQTGSHPGRLAGRWLWGAQPCLLPIVPLSLWMLLLLLLLASLLPSARLASPLPREE 60
 QY 61 IVFPEKLSVLPFGSGAPARLLCRLOAFGETLLLEQDSGVQVEGLTVQYLQAPPELLG 120
 DB 61 IVFPEKLSVLPFGSGAPARLLCRLOAFGETLLLEQDSGVQVEGLTVQYLQAPPELLG 120
 QY 121 GAEPGYLTGTINGDPESVSLHWDGALLGVLYRGAELHQLPREGTSPNSAGGPAH 180
 DB 121 GAEPGYLTGTINGDPESVSLHWDGALLGVLYRGAELHQLPREGTSPNSAGGPAH 180
 QY 181 LRKSPASGGPCNWKAPLGSPPRPRAKRPAFLSRFVETLVVADDDKMAFPHGAGLKR 240
 DB 181 LRKSPASGGPCNWKAPLGSPPRPRAKRPAFLSRFVETLVVADDDKMAFPHGAGLKR 240
 QY 241 YLTVMAAAKAPKPSIRNPVSLVTRVLVILSGEGEPQVGPSSAAQTLSRSCAWORGLN 300
 DB 241 YLTVMAAAKAPKPSIRNPVSLVTRVLVILSGEGEPQVGPSSAAQTLSRSCAWORGLN 300
 QY 301 TPEDSDPDHEDTALLTFRODLQGVSTCDTLGMADVGTVCDDPARSCAIVDDGLQSAFTAA 360
 DB 301 TPEDSDPDHEDTALLTFRODLQGVSTCDTLGMADVGTVCDDPARSCAIVDDGLQSAFTAA 360
 QY 361 HELGHVFNMLHDSKPCISLNGPLSTRHVMFVMAHVDPEEPWSPCSARFIFDLDNGY 420
 DB 361 HELGHVFNMLHDSKPCISLNGPLSTRHVMFVMAHVDPEEPWSPCSARFIFDLDNGY 420
 QY 421 GHCLLDKPEAPLHLVTPFGKYDADRQCQLTFGPDSPRHCPQLPPCAALWCSCGLNGHA 480
 DB 421 GHCLLDKPEAPLHLVTPFGKYDADRQCQLTFGPDSPRHCPQLPPCAALWCSCGLNGHA 480
 QY 481 MCOTKHSPPWADGTPCGPAQACMGRCILHMDLODENIPQAGGWPWGPWGDSCSRTCGGV 540
 DB 481 MCOTKHSPPWADGTPCGPAQACMGRCILHMDLODENIPQAGGWPWGPWGDSCSRTCGGV 540
 QY 541 QFSRSDCTRPVPRNGKYGCEGRTRFRSCNTECPTGSALTFRFEECAAYNHRITLTKSF 600
 DB 541 QFSRSDCTRPVPRNGKYGCEGRTRFRSCNTECPTGSALTFRFEECAAYNHRITLTKSF 600
 QY 601 PGPMDWPRVTGVAPOQCKLTQARALGYVYVLEPRVDGTPCSPDSSVCVQGRCIHA 660
 DB 601 PGPMDWPRVTGVAPOQCKLTQARALGYVYVLEPRVDGTPCSPDSSVCVQGRCIHA 660
 QY 661 GCDRIIGSKKKFKDKMVCVGGSGCSKQSGFRKRYGYNVVTIPAGATHILVROQGNP 720
 DB 661 GCDRIIGSKKKFKDKMVCVGGSGCSKQSGFRKRYGYNVVTIPAGATHILVROQGNP 720
 QY 721 GHSIYLALKLPDGSYALNGEYTLMPSTVDVLPFGAVSLRYSGATASETLSHGHPAQ 780
 DB 721 GHSIYLALKLPDGSYALNGEYTLMPSTVDVLPFGAVSLRYSGATASETLSHGHPAQ 780
 QY 781 LTLQVLVAGNPQDTRLYSFVFRPTPTSPRPTQDMLHRRRAQILEILRRRPPWAGRK 837
 DB 781 LTLQVLVAGNPQDTRLYSFVFRPTPTSPRPTQDMLHRRRAQILEILRRRPPWAGRK 837

RESULT 2
 ADJ69542
 ID ADJ69542 standard; protein; 837 AA.
 AC ADJ69542;
 DT 06-MAY-2004 (first entry)
 XX Human heat mitochondrial protein as a therapeutic target SeqID1348.
 KW mitochondrial; human; screening assay; diabetes mellitus;
 KW Huntington's disease; osteoarthritis;
 KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cytostatic.
 OS Homo sapiens.
 XX WO2003087768-A2.
 XX 23-OCT-2003.
 XX 04-APR-2003; 2003WO-US010870.
 XX 12-APR-2002; 2002US-0372843P.
 XX 17-JUN-2002; 2002US-0389987P.
 XX 20-SEP-2002; 2002US-0412418P.
 XX (MITO-) MITOKOR.
 XX (BUCK-) BUCK INST AGE RES.
 XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 XX Warnock DE;
 XX WPI; 2003-845369/78.
 XX Identifying a mitochondrial target for drug screening assays and for
 XX treating diseases associated with altered mitochondrial function,
 XX PT comprises detecting a modified polypeptide in a sample and correlating
 XX with the disease.
 XX Claim 1; SEQ ID NO 1348; 180pp; English.
 XX This invention relates to novel mitochondrial targets that can be used
 XX for therapeutic intervention in treating a disease associated with
 XX altered mitochondrial function. Specifically, it refers to a method for
 XX identifying proteins of the human heart mitochondrial proteome that are
 XX useful for drug screening assays, as well as therapeutic targets. The
 XX present invention describes a method for identifying such proteins that
 XX can be used in the treatment of various diseases associated with altered
 XX mitochondrial function including diabetes mellitus, Huntington's disease,
 XX osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 XX encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 XX ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 XX compositions have neuroprotective, nontropic, antidiabetic,
 XX anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 XX cytostatic activities. This polypeptide sequence is a human heart
 XX mitochondrial protein of the invention.
 XX Sequence 837 AA;

Query Match 100.0%; Score 4570; DB 7; Length 837;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 837; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQTGSHPGRLAGRWLWGAQPCLLPIVPLSLWMLLLLLLLASLLPSARLASPLPREE 60
 DB 1 MSQTGSHPGRLAGRWLWGAQPCLLPIVPLSLWMLLLLLLLASLLPSARLASPLPREE 60
 QY 61 IVFPEKLSVLPFGSGAPARLLCRLOAFGETLLLEQDSGVQVEGLTVQYLQAPPELLG 120

Db 61 IVPPEKLSVLPFGSGAPARLLCRLOAFGETLLELEQDSGVQVEGLTVQYLGQAPELIG 120
QY 121 GAEPTGLTGTINGDPESVASLHWDGALLGVYRGAEHLHLOPLEGGTPNSAGPGAH 180
Db 121 GAEPTGLTGTINGDPESVASLHWDGALLGVYRGAEHLHLOPLEGGTPNSAGPGAH 180
QY 181 LRKSPASGGPWCNVKAPLPGSPSPRRPRAKRPAFLSRFVETLVVADDDKAAAFHGAGLKR 240
Db 181 LRKSPASGGPWCNVKAPLPGSPSPRRPRAKRPAFLSRFVETLVVADDDKAAAFHGAGLKR 240
QY 241 YLLTMAAAAKAFKPSIRNPVSLVTRVLVILGSBEGPQVGPSSAQTLSFCQWQGLN 300
Db 241 YLLTMAAAAKAFKPSIRNPVSLVTRVLVILGSBEGPQVGPSSAQTLSFCQWQGLN 300
QY 301 TPEDSDPHDFTAILFTRODLGVSTCDTLGMADVGTCDPARSCAIVEDDDGLQSAFTAA 360
Db 301 TPEDSDPHDFTAILFTRODLGVSTCDTLGMADVGTCDPARSCAIVEDDDGLQSAFTAA 360
QY 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAPVMAHVDPEEPWSPCSARFITDLDNGY 420
Db 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAPVMAHVDPEEPWSPCSARFITDLDNGY 420
QY 421 GHCLLDKPEAPLHLPVTFPGKYDADRQCLTFGPDSDRHCPOLPDPPCAALWCSGHLNGHA 480
Db 421 GHCLLDKPEAPLHLPVTFPGKYDADRQCLTFGPDSDRHCPOLPDPPCAALWCSGHLNGHA 480
QY 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWPMPGDCSRTCGGV 540
Db 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWPMPGDCSRTCGGV 540
QY 541 QFSRDCTRPVPRNGSKYCEGRTRFRSCNTEDCPTGSALTFRBQCAAYNHRITDLKSF 600
Db 541 QFSRDCTRPVPRNGSKYCEGRTRFRSCNTEDCPTGSALTFRBQCAAYNHRITDLKSF 600
QY 601 PGPMWVPRYTGVAPQDQCKLTCQALGYVYVLEPRVVDGTPCPDSSVVCQRCIHA 660
Db 601 PGPMWVPRYTGVAPQDQCKLTCQALGYVYVLEPRVVDGTPCPDSSVVCQRCIHA 660
QY 661 GCDRIIGSKKFDKCMVCGDGGSGSKSGSRKRYGNNVVTIPAGATHILVQQGNP 720
Db 661 GCDRIIGSKKFDKCMVCGDGGSGSKSGSRKRYGNNVVTIPAGATHILVQQGNP 720
QY 721 GHSIYLALKLPDGSVALNGEYTLMPSTDDVVLPGAVSLRYSGATAASETLSGHGFLAQP 780
Db 721 GHSIYLALKLPDGSVALNGEYTLMPSTDDVVLPGAVSLRYSGATAASETLSGHGFLAQP 780
QY 781 LTQLVLVAGNPQDRLRYSFFVPRPTPPTPDQDLHRRQAQILEILRRRPPWAGRK 837
Db 781 LTQLVLVAGNPQDRLRYSFFVPRPTPPTPDQDLHRRQAQILEILRRRPPWAGRK 837

RESULT 3
ADS20209

ID ADS20209 standard; protein; 837 AA.

AC ADS20209;

DT 18-NOV-2004 (first entry)

DE Human aggrecanase ADAMTS4 pro-protein.

XX ADAMTS4; a disintegrin-like and metalloprotease;
KW thrombospondin type 1 motif 4; reprotysin; zinc metalloprotease;
KW aggrecanase; osteoarthritis; antiinflammatory; antiarthritic; antirheumatic;
KW cytostatic; osteoarthritis; glioma; cancer; inflammatory joint;
KW rheumatoid arthritis; septic arthritis; periodontal; Crohn's disease;
KW human; pro-protein; chromosome 1q21-q23; enzyme.

OS Homo sapiens.

XX Key Location/Qualifiers
FH 1. .212
FT Peptide

FT Domain /note= "Pro-peptide"
213. .436
FT Domain /note = Metalloproteinase catalytic domain
437. .519
FT Domain /note = Disintegrin-like domain
520. .576
FT Domain /note = TSP-1 (thrombospondin type I) motif
577. .685
FT Domain /note = Cysteine-rich domain
581. .582
FT Cleavage-site /note="Auto-digestion cleavage site"
686. .837
FT Domain /note = Spacer domain
694. .695
FT Cleavage-site /note= "Auto-digestion cleavage site"

WO2004011637-A2.

PN 05-FEB-2004.

XX 29-JUL-2003; 2003WO-US023484.

XX 29-JUL-2002; 2002US-0398721P.

XX (AMHP) WYETH.

PA (CORC/) CORCORAN C J.

PA (FLAN/) FLANNERY C R.

PA (ZENG/) ZENG W.

PA (RACI/) RACIE L A.

PA (MCD/) MCDONAGH T.

PA (FREE/) FREEMAN B A.

PA (GEOR/) GEORGADIS K E.

PA (LAVA/) LAVALLIE B R.

PI Corcoran CJ, Flannery CR, Zeng W, Racie LA, Mcdonagh T;

PI Freeman BA, Georgiadis KE, Lavallie ER;

XX WPI; 2004-143860/14.

XX New isolated, modified ADAMTS4 (aggrecanase) protein with improved
PT stability useful for identifying inhibitors of the enzyme activity for
PT treating aggrecanase-associated conditions, including osteoarthritis.

PS Example 6; SEQ ID NO 1; 117pp; English.

XX The invention relates to a novel isolated, modified ADAMTS4 (a

CC disintegrin-like and metalloprotease (reprotysin type) with

CC thrombospondin type 1 motif 4) protein with improved stability compared

CC to a naturally occurring, full-length ADAMTS4 protein, where the modified

CC protein differs from the naturally-occurring, full-length ADAMTS4 protein

CC by at least one amino acid. ADAMTS proteins are a subfamily of zinc

CC metalloproteases and include aggrecanases amongst their members. The

CC protein of the invention demonstrates osteopathic, antiinflammatory,

CC antiarthritic, antirheumatic and cytostatic activities and may be useful

CC for treating aggrecanase-associated conditions, including osteoarthritis,

CC glioma, cancer, inflammatory joint disease, rheumatoid arthritis, septic

CC arthritis, periodontal disease and Crohn's disease. The current sequence

CC is that of the human aggrecanase ADAMTS4 pro-protein of the invention

CC which is encoded by DNA located at chromosome 1q21-q23.

XX Sequence 837 AA;

Query Match 100.0%; Score 4570; DB 8; Length 837;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 837; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQTGSHPGRLAGRWLWGAQPCLLLPVPSLWLLVLLLLASLLPSARLASPLPREE 60

Db 1 MSQTGSHPGRLAGRWLWGAQPCLLLPVPSLWLLVLLLLASLLPSARLASPLPREE 60

QY 61 IVFPPEKLSVLPFGSGAPARLLCRLOAFGETLLELEQDSGVQVEGLTVQYLGQAPELIG 120

Db 61 IVFPPEKLSVLPFGSGAPARLLCRLOAFGETLLELEQDSGVQVEGLTVQYLGQAPELIG 120

QY	121	GAEPGYLTGTTINGDPESVASLHWDGALLGVLYRGAEHLQPLEGGTPNSAGGPGAH	180
DB	121	GAEPGYLTGTTINGDPESVASLHWDGALLGVLYRGAEHLQPLEGGTPNSAGGPGAH	180
QY	181	LRKSPASGOGPMCNVKAFLGSPSPRRAKRPFASLSRFVETLVADDDKMAAFHGAGLKR	240
DB	181	LRKSPASGOGPMCNVKAFLGSPSPRRAKRPFASLSRFVETLVADDDKMAAFHGAGLKR	240
QY	241	YLLTVMMAAAKAFKHPISIRNPVSLVTRVLVILSGEGEPQVGPSSAAQTILRSFCAWORGLN	300
DB	241	YLLTVMMAAAKAFKHPISIRNPVSLVTRVLVILSGEGEPQVGPSSAAQTILRSFCAWORGLN	300
QY	301	TPEDSPDHPDTHAILTRQDLQGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAA	360
DB	301	TPEDSPDHPDTHAILTRQDLQGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAA	360
QY	361	HELGHVFNMLHDSKPCISLNGPLSTSRHVMAFVMAHVDPEEPWSPCSARFIFDLDNGY	420
DB	361	HELGHVFNMLHDSKPCISLNGPLSTSRHVMAFVMAHVDPEEPWSPCSARFIFDLDNGY	420
QY	421	GHCLLDKPEAPLHLPVTFPGKYDADRQCQLTFGPDSPHCPQLPPPCAAALWCSGHLNGHA	480
DB	421	GHCLLDKPEAPLHLPVTFPGKYDADRQCQLTFGPDSPHCPQLPPPCAAALWCSGHLNGHA	480
QY	481	MCQTKSPWADGTPCGPAQACMGRCCLHMDLODFNIPOAGGWGMPGDCSRTCGGV	540
DB	481	MCQTKSPWADGTPCGPAQACMGRCCLHMDLODFNIPOAGGWGMPGDCSRTCGGV	540
QY	541	QFSRDCTRPVPRNGGKYCEGRTRFRSCNTECDPTGSALTFRFEEQCAAYNHRITDLFKSF	600
DB	541	QFSRDCTRPVPRNGGKYCEGRTRFRSCNTECDPTGSALTFRFEEQCAAYNHRITDLFKSF	600
QY	601	PGPMWVPRVTGVAPOQCKLTQCARALGYVYVLEPRVDGTGTPCSPDSSVCVQGRCIHA	660
DB	601	PGPMWVPRVTGVAPOQCKLTQCARALGYVYVLEPRVDGTGTPCSPDSSVCVQGRCIHA	660
QY	661	GCDRIIGSKKKFKDKMVCWGDSGSCSKQSPKFRGYNNVVTIPAGATHILVROQGNP	720
DB	661	GCDRIIGSKKKFKDKMVCWGDSGSCSKQSPKFRGYNNVVTIPAGATHILVROQGNP	720
QY	721	GHSIYLALXLPDGSYALNGEYTIMPSPTDVLPGAVSLRYSGATAASETLSHGFLAQP	780
DB	721	GHSIYLALXLPDGSYALNGEYTIMPSPTDVLPGAVSLRYSGATAASETLSHGFLAQP	780
QY	781	LTLQVLVAGNPQDTRLYSFVFRPTSTPRTPQDWLHRAQILEILRRPWRGRK	837
DB	781	LTLQVLVAGNPQDTRLYSFVFRPTSTPRTPQDWLHRAQILEILRRPWRGRK	837
RESULT 4			
ADS20232			
ID	ADS20232	standard; protein; 846 AA.	
AC	XX		
AC	XX		
AC	XX		
DT	18-NOV-2004	(first entry)	
DE	XX	Human aggrecanase ADAMTS4 mutant E362Q protein with FLAG tag.	
DE	XX		
KW	XX	ADAMTS4; a disintegrin-like and metalloprotease;	
KW	XX	thrombospondin type 1 motif 4; reprotolysin; zinc metalloprotease;	
KW	XX	aggrecanase; osteopontin; antiinflammatory; antiarthritic; antirheumatic;	
KW	XX	cytosolic; osteoarthritis; glioma; cancer; inflammatory joint;	
KW	XX	rheumatoid arthritis; septic arthritis; periodontal; Crohn's disease;	
KW	XX	human; enzyme; chromosome 1q21-q23; FLAG tag; mutant; mutin.	
OS	XX	Homo sapiens.	
OS	XX	Synthetic.	
Key		Location/Qualifiers	
FH	362		
FT		Misc-difference 362	
FT		/note= "Wild-type Glu substituted by Gln"	

FT		Misc-difference 838. .846	
FT		/note= "FLAG tag"	
XX			
PN	WO2004011637-A2.		
XX			
PD	05-FEB-2004.		
XX			
PF	29-JUL-2003; 2003WO-US023484.		
XX			
PR	29-JUL-2002; 2002US-0398721P.		
XX	(AMHP) WYETH.		
PA	(CORC/) CORCORAN C J.		
PA	(FLAN/) FLANNERY C R.		
PA	(ZENG/) ZENG W.		
PA	(RACI/) RACIE L A.		
PA	(MCDO/) MCDONAGH T.		
PA	(FREE/) FREEMAN B A.		
PA	(GEOR/) GEORGIADIS K E.		
PA	(LAVA/) LAVALLIE E R.		
XX			
PI	Corcoran CJ, Flannery CR, Zeng W, Racie LA, Mcdonagh T;		
PI	Freeman BA, Georgiadis KE, Lavallie ER;		
XX			
DR	WPI; 2004-143860/14.		
XX			
PT	New isolated, modified ADAMTS4 (aggrecanase) protein with improved		
PT	stability useful for identifying inhibitors of the enzyme activity for		
PT	treating aggrecanase-associated conditions, including osteoarthritis.		
XX			
PS	Claim 9; SEQ ID NO 29; 117pp; English.		
XX			
CC	The invention relates to a novel isolated, modified ADAMTS4 (a		
CC	disintegrin-like and metalloprotease (reprotolysin type) with		
CC	thrombospondin type 1 motif 4) protein with improved stability compared		
CC	to a naturally occurring, full-length ADAMTS4 protein, where the modified		
CC	protein differs from the naturally-occurring, full-length ADAMTS4 protein		
CC	by at least one amino acid. ADAMTS proteins are a subfamily of zinc		
CC	metalloproteases and include aggrecanases amongst their members. The		
CC	protein of the invention demonstrates osteopontin, antiinflammatory,		
CC	antiarthritic, antirheumatic and cytostatic activities and may be useful		
CC	for treating aggrecanase-associated conditions, including osteoarthritis,		
CC	glioma, cancer, inflammatory joint disease, rheumatoid arthritis, septic		
CC	arthritis, periodontal disease and Crohn's disease. The current sequence		
CC	is that of the human aggrecanase ADAMTS4 mutant E362Q protein with FLAG		
CC	tag of the invention.		
XX			
SQ	Sequence 846 AA;		
	Query Match 99.9%; Score 4567; DB 8; Length 846;		
	Best Local Similarity 99.9%; Pred. No. 0;		
	Matches 836; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
QY	1	MSQTGSHPGRLAGRWLWGAQPCLLPIVPLSWLWLLLLASLPSARLASPLPREEE	60
DB	1	MSQTGSHPGRLAGRWLWGAQPCLLPIVPLSWLWLLLLASLPSARLASPLPREEE	60
QY	61	IYFPEKLSVLPVPGSGAPARLLCRLOAFQGTLLLEQDSGVQVEGLTVQYLGAPELLG	120
DB	61	IYFPEKLSVLPVPGSGAPARLLCRLOAFQGTLLLEQDSGVQVEGLTVQYLGAPELLG	120
QY	121	GAEPGYLTGTTINGDPESVASLHWDGALLGVLYRGAEHLQPLEGGTPNSAGGPGAH	180
DB	121	GAEPGYLTGTTINGDPESVASLHWDGALLGVLYRGAEHLQPLEGGTPNSAGGPGAH	180
QY	181	LRKSPASGOGPMCNVKAFLGSPSPRRAKRPFASLSRFVETLVADDDKMAAFHGAGLKR	240
DB	181	LRKSPASGOGPMCNVKAFLGSPSPRRAKRPFASLSRFVETLVADDDKMAAFHGAGLKR	240
QY	241	YLLTVMMAAAKAFKHPISIRNPVSLVTRVLVILSGEGEPQVGPSSAAQTILRSFCAWORGLN	300
DB	241	YLLTVMMAAAKAFKHPISIRNPVSLVTRVLVILSGEGEPQVGPSSAAQTILRSFCAWORGLN	300

QY 301 TPEDSDPHDFTAILTRDQLCGVSTCDTLGNADVTCVCDPARSCAIVEDDGLQSAFTAA 360
Db TPEDSDPHDFTAILTRDQLCGVSTCDTLGNADVTCVCDPARSCAIVEDDGLQSAFTAA 360
QY 361 HELGHVFNMLHNSKPCISLNGPLSTRSHVMAVMAHVDPPEPWPSCSARFITDFLDNGY 420
Db HQHGHVFNMLHNSKPCISLNGPLSTRSHVMAVMAHVDPPEPWPSCSARFITDFLDNGY 420
QY 421 GHCLLDKPEAPLHLVPTFFGKDYADROQCLTFGPDSDRHCPCOLPPPCAALWCSGHLNGHA 480
Db GHCLLDKPEAPLHLVPTFFGKDYADROQCLTFGPDSDRHCPCOLPPPCAALWCSGHLNGHA 480
QY 481 MCQTKHSPWADGTPCGPAQACMGGRCLHMDQLQDFNIPOAGGKWPMPGDCSRTCCGGV 540
Db MCQTKHSPWADGTPCGPAQACMGGRCLHMDQLQDFNIPOAGGKWPMPGDCSRTCCGGV 540
QY 541 QFSRRDCTRPVPRNGGKYCEGRTRFRSCNTEDCPTGSALTFRFEECAAYNHRITDLFKSF 600
Db QFSRRDCTRPVPRNGGKYCEGRTRFRSCNTEDCPTGSALTFRFEECAAYNHRITDLFKSF 600
QY 601 PGPMWVPRYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSVCVQGRCIHA 660
Db PGPMWVPRYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSVCVQGRCIHA 660
QY 661 GCDRIIGSKKXKFDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQGNP 720
Db GCDRIIGSKKXKFDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQGNP 720
QY 721 GHRISYLALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAAETLSGHGFLAQP 780
Db GHRISYLALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAAETLSGHGFLAQP 780
QY 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPTPDQWLHRRRAQIILEILRRRPWAGRK 837
Db LTLQVLVAGNPQDTRLRYSFVPRPTPTPTPDQWLHRRRAQIILEILRRRPWAGRK 837

RESULT 5
AAG78228

ID AAG78228 standard; protein; 837 AA.
XX AC AAG78228;
XX DT 13-DEC-2001 (first entry)
XX DE Human aggrecanase-1 SEQ ID NO 3.
XX KW Human; aggrecanase-1; ADAMTS4; promoter; antiarthritic.
XX OS Homo sapiens.
XX PN JP2001245663-A.
XX PD 11-SEP-2001.
XX PF 06-MAR-2000; 2000JP-00059952.
XX PR 06-MAR-2000; 2000JP-00059952.
XX PA (EISA) EISAI CO LTD.
XX WPI; 2001-610072/70.
XX DR N-PSDB; AAI68146.
XX

New DNA for use as a promoter for controlling the expression of aggrecanase-1.

Disclosure; Page 9-11; 12pp; Japanese.

CC The invention relates to a DNA acting as a promoter controlling the expression of aggrecanase-1 (ADAMTS4) resulting in antiarthritic activity. The DNA is used in a method for screening a compound affecting the expression control of the aggrecanase-1 gene

XX Sequence 837 AA;

Query Match 99.9%; Score 4566; DB 4; Length 837;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSQTSQSHPGRLAGRLWMAQPCLLLPVPLSWLWMLLLLLASLLPSARLASPLPREE 60
Db 1 MSQTSQSHPGRLAGRLWMAQPCLLLPVPLSWLWMLLLLLASLLPSARLASPLPREE 60
QY 61 IVFPEKLSGVLPGSGAPARLLCRLOAFGETLLLEQDSGVQVEGLTVQYLQAPBELLG 120
Db 61 IVFPEKLSGVLPGSGGTPARLLCRLOAFGETLLLEQDSGVQVEGLTVQYLQAPBELLG 120
QY 121 GAEPGTYYLTGTINGDPESVASLHWDGGLLVQLVYRGAEHLQPLEGGTPNSAGGGAHI 180
Db 121 GAEPGTYYLTGTINGDPESVASLHWDGGLLVQLVYRGAEHLQPLEGGTPNSAGGGAHI 180
QY 181 LRRKSPASQGGPMCNVKAFLGSPSPRRRAKFAFASLSRFVETLVVADDDKMAAFHGAGLK 240
Db 181 LRRKSPASQGGPMCNVKAFLGSPSPRRRAKFAFASLSRFVETLVVADDDKMAAFHGAGLK 240
QY 241 YLLTWMAAAKAFKHPSTRNPVSLVTRLVILSGEPEGVQGPSAAQTILRSPFCAMORGLN 300
Db 241 YLLTWMAAAKAFKHPSTRNPVSLVTRLVILSGEPEGVQGPSAAQTILRSPFCAMORGLN 300
QY 301 TPEDSDPHDFTAILTRDQLCGVSTCDTLGNADVTCVCDPARSCAIVEDDGLQSAFTAA 360
Db 301 TPEDSDPHDFTAILTRDQLCGVSTCDTLGNADVTCVCDPARSCAIVEDDGLQSAFTAA 360
QY 361 HELGHVFNMLHNSKPCISLNGPLSTRSHVMAVMAHVDPPEPWPSCSARFITDFLDNGY 420
Db 361 HELGHVFNMLHNSKPCISLNGPLSTRSHVMAVMAHVDPPEPWPSCSARFITDFLDNGY 420
QY 421 GHCLLDKPEAPLHLVPTFFGKDYADROQCLTFGPDSDRHCPCOLPPPCAALWCSGHLNGHA 480
Db 421 GHCLLDKPEAPLHLVPTFFGKDYADROQCLTFGPDSDRHCPCOLPPPCAALWCSGHLNGHA 480
QY 481 MCQTKHSPWADGTPCGPAQACMGGRCLHMDQLQDFNIPOAGGKWPMPGDCSRTCCGGV 540
Db 481 MCQTKHSPWADGTPCGPAQACMGGRCLHMDQLQDFNIPOAGGKWPMPGDCSRTCCGGV 540
QY 541 QFSRRDCTRPVPRNGGKYCEGRTRFRSCNTEDCPTGSALTFRFEECAAYNHRITDLFKSF 600
Db 541 QFSRRDCTRPVPRNGGKYCEGRTRFRSCNTEDCPTGSALTFRFEECAAYNHRITDLFKSF 600
QY 601 PGPMWVPRYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSVCVQGRCIHA 660
Db 601 PGPMWVPRYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSVCVQGRCIHA 660
QY 661 GCDRIIGSKKXKFDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQGNP 720
Db 661 GCDRIIGSKKXKFDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQGNP 720
QY 721 GHRISYLALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAAETLSGHGFLAQP 780
Db 721 GHRISYLALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAAETLSGHGFLAQP 780
QY 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPTPDQWLHRRRAQIILEILRRRPWAGRK 837
Db 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPTPDQWLHRRRAQIILEILRRRPWAGRK 837

RESULT 6
ADB85488

ID ADB85488 standard; protein; 837 AA.
XX AC ADB85488;
XX DT 04-DEC-2003 (first entry)
XX DE Human aggrecanase-1 (ADAMTS-4) wild-type protein sequence.

XX aggrecanase; aggrecan; articular cartilage; proteoglycan; cartilage compressibility; cartilage elasticity; arthritic disease; osteoarthritis; cartilage degradation; inflammatory joint disease; aggrecanase-1; ADAMTS-4; aggrecanase-2; ADAMTS-5; thrombospondin domain; TSP domain; osteopontin; antiarthritic; cytoskeletal; antiinflammatory; antineuritic; ophthalmological; thrombolytic; vasotropic; antimicrobial; respiratory-gen; neutropenic; neuroprotective; antiparkinsonian; immunosuppressive; aggrecanase inhibition; cancer; rheumatoid arthritis; septic arthritis; corneal ulceration; coronary thrombosis; Crohn's disease; emphysema; Alzheimer's disease; Parkinson's disease; multiple sclerosis; aortic aneurysm; enzyme; human.

XX Homo sapiens.

XX WO2003066822-A2.

XX 14-AUG-2003.

XX 05-FEB-2003; 2003WO-US003554.

XX 05-FEB-2002; 2002US-0354592P.

XX (AMHP) WYETH.

XX Georgiadis K, Crawford TK, Tomkinson KN, Morris EA, Racie L;

XX WPI; 2003-731495/69.

XX N-PSDB; ADB85504.

XX New biologically-active aggrecanase protein having a deletion of all, or a portion of a TSP domain, useful for treating osteoarthritis, cancer, Parkinson's disease, coronary thrombosis, Alzheimer's disease and multiple sclerosis.

XX Disclosure; Fig 11; 11lpp; English.

XX This invention relates to novel truncated human aggrecanase proteins and nucleotide sequences. Aggrecan is a major extracellular component of articular cartilage. It is a proteoglycan responsible for providing cartilage with its mechanical properties of compressibility and elasticity. The loss of aggrecan has been implicated in the degradation of articular cartilage in arthritic diseases such as osteoarthritis. Aggrecanase is responsible for the cleavage of aggrecan, thereby having a role in cartilage degradation associated with osteoarthritis and inflammatory joint disease. The proteins of the current invention are truncated aggrecanase-1 (ADAMTS-4) and aggrecanase-2 (ADAMTS-5) enzymes which have at least one thrombospondin (TSP) domain deleted. These are biologically active and have greater stability and higher expression than their full-length counterparts. The proteins of the invention may be of use in the development of compounds with osteopathic, antiarthritic, cytoskeletal, antiinflammatory, antineuritic, ophthalmological, thrombolytic, vasotropic, antimicrobial, respiratory-gen, neutropenic, neuroprotective, antiparkinsonian or immunosuppressive activities through aggrecanase inhibition. The proteins of the invention may therefore be useful for the manufacture of compositions for the treatment of aggrecanase-associated conditions, such as osteoarthritis, cancer, inflammatory joint disease, rheumatoid arthritis, septic arthritis, corneal ulceration, coronary thrombosis, Crohn's disease, emphysema, Alzheimer's disease, Parkinson's disease, multiple sclerosis and aortic aneurysm. The present sequence is the full-length amino acid sequence of the aggrecanase-1 (ADAMTS-4) enzyme which was used to create the truncated aggrecanase-1 proteins of the invention.

XX Sequence 837 AA;

XX Query Match 99.9%; Score 4566; DB 7; Length 837;

XX Best Local Similarity 99.9%; Pred. No. 0;

XX Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX 1 MSQTSHPGRGLAGRWLGAQPCLLPIVPLSWLWLLILLASLLPSARLASPLPREEE 60

XX 1 MSQTSHPGRGLAGRWLGAQPCLLPIVPLSWLWLLILLASLLPSARLASPLPREEE 60

QY 61 IVFEKLNGSVLPGSGAPARLLCRLOAFGETLLELEQDSGVQVEGLTVQVLOAPELLG 120

DB 61 IVFEKLNGSVLPGSGAPARLLCRLOAFGETLLELEQDSGVQVEGLTVQVLOAPELLG 120

QY 121 GAEPGYTLTGTINGDPESVASLHWGGALLGVQVYRGAEHLQPLEGGTPNSAGPGAH 180

DB 121 GAEPGYTLTGTINGDPESVASLHWGGALLGVQVYRGAEHLQPLEGGTPNSAGPGAH 180

QY 181 LRRKSPASGQGMCMNVKAPLSPSPRRKRFRASLRFVETLVVADDKMAAFHAGLGR 240

DB 181 LRRKSPASGQGMCMNVKAPLSPSPRRKRFRASLRFVETLVVADDKMAAFHAGLGR 240

QY 241 YLLTWMAAAAKAFKHPISIRNPVSLVTLVILSGEGEPQVGSAAQTLRSCAWORGLN 300

DB 241 YLLTWMAAAAKAFKHPISIRNPVSLVTLVILSGEGEPQVGSAAQTLRSCAWORGLN 300

QY 301 TPEDSDPDHFDTAILFTQDLGCVSTCTGLMADVTVCDPARSCAIVEDDGLQSAFTAA 360

DB 301 TPEDSDPDHFDTAILFTQDLGCVSTCTGLMADVTVCDPARSCAIVEDDGLQSAFTAA 360

QY 361 HELGHVFNMLHDNSKPCISLNGPLSTSRHMAPVMAHVDPEPWPSPCSARFITDLDNGY 420

DB 361 HELGHVFNMLHDNSKPCISLNGPLSTSRHMAPVMAHVDPEPWPSPCSARFITDLDNGY 420

QY 421 GHCLLDKPEAPLHLPVTFPGKDYDADRCQCLTFPGDSRHCPQLPPCAALMCSGHLNGHA 480

DB 421 GHCLLDKPEAPLHLPVTFPGKDYDADRCQCLTFPGDSRHCPQLPPCAALMCSGHLNGHA 480

QY 481 MCQTKHSPWADTGPCGPAQACMGGRCLHMDQLQDNIIPOAGGWPWGMDGDCSRCTCGGV 540

DB 481 MCQTKHSPWADTGPCGPAQACMGGRCLHMDQLQDNIIPOAGGWPWGMDGDCSRCTCGGV 540

QY 541 QFSSRDCTRPVPRNGSKYCEGRTRFRSCNTDCTGSGALTFRPQCAAYNHTDLFKSF 600

DB 541 QFSSRDCTRPVPRNGSKYCEGRTRFRSCNTDCTGSGALTFRPQCAAYNHTDLFKSF 600

QY 601 PGFMDWVPRYTGVAPQDQCKLFCQARALGYVYVLPFRVVDGTPCSPDSSSVQCRCIHA 660

DB 601 PGFMDWVPRYTGVAPQDQCKLFCQARALGYVYVLPFRVVDGTPCSPDSSSVQCRCIHA 660

QY 661 GCDRIIGSKKPKDKMVCGGGSGSKSGSKGSKGSKGSKGSKGSKGSKGSKGSKGSKGSKG 720

DB 661 GCDRIIGSKKPKDKMVCGGGSGSKSGSKGSKGSKGSKGSKGSKGSKGSKGSKGSKGSKG 720

QY 721 GHSIYVIALKLPDGSVALNGEYTLMPSPDTPVLPVAVSLRYSGLATAAETLSGHGPLAOP 780

DB 721 GHSIYVIALKLPDGSVALNGEYTLMPSPDTPVLPVAVSLRYSGLATAAETLSGHGPLAOP 780

QY 781 LTLQVLVAGNPQDTRLYRFFVPRTPPTPPTPQDHLHRAQILILRRRPPWAGRK 837

DB 781 LTLQVLVAGNPQDTRLYRFFVPRTPPTPPTPQDHLHRAQILILRRRPPWAGRK 837

RESULT 7

AAAB21256

ID AAAB21256 standard; protein; 840 AA.

XX AAAB21256;

AC AAAB21256;

XX 23-FEB-2001 (first entry)

DE Human metalloproteinase KIAA0688.

XX Human; KIAA0688; metalloproteinase; ADAM;

XX a disintegrin and metalloproteinase domain; thrombospondin domain;

XX vaccine; neutropenic; neuroprotective; antiparkinsonian; cerebrotective;

XX cytoskeletal; antiarthritic; immunosuppressive; Alzheimer's disease;

XX Parkinson's disease; stroke; cancer; arthritis; autoimmune disease;

XX brain tumour; brain injury.

XX Homo sapiens.

Fri Apr 1 15:02:39 2005

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PR 17-SEP-1998; 98US-0100584P.
PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100848P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101471P.
PR 22-SEP-1998; 98US-0101472P.
PR 22-SEP-1998; 98US-0101474P.
PR 22-SEP-1998; 98US-0101475P.
PR 22-SEP-1998; 98US-0101476P.
PR 22-SEP-1998; 98US-0101477P.
PR 22-SEP-1998; 98US-0101479P.
PR 22-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101741P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101915P.
PR 24-SEP-1998; 98US-0101916P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102307P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102484P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-0103314P.
PR 07-OCT-1998; 98US-0103315P.
PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103395P.
PR 07-OCT-1998; 98US-0103396P.
PR 07-OCT-1998; 98US-0103401P.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103719P.
PR 08-OCT-1998; 98US-0103719P.
PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105000P.
PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105693P.
PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106062P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.

PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 18-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108859P.
PR 18-NOV-1998; 98US-0108904P.

PA (GETH ) GENENTECH INC.
PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
DR WPI; 2000-237871/20.
XX N-PSDB; AAA37111.
XX
XX New mammalian DNA sequences encoding transmembrane, receptor or secreted
PT PRO polypeptides, useful for screening of potential peptide or small
PT molecule inhibitors of the relevant receptor/ligand interactions.
XX
XX Claim 12; Fig 180; 773pp; English.
XX
XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
CC transmembrane and receptor PRO proteins can be used for screening of
CC potential peptide or small molecule inhibitors of the relevant
CC receptor/ligand interactions. The polypeptides and nucleotide sequences
CC encoding then have various industrial applications, including uses as
CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
CC primers and hybridisation probes used in the isolation of the PRO
CC polypeptides from the present invention
XX
XX Sequence 837 AA;
SQ

Query Match 99.8%; Score 4563; DB 3; Length 837;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSQTGSHPGRLAGRWLWGAQPCLLLPIVPLSLWLVWLLLLLLASLLPSARLASPLPREEE 60
Db 1 MSQTGSHPGRLAGRWLWGAQPCLLLPIVPLSLWLVWLLLLLLASLLPSARLASPLPREEE 60
QY 61 IVFPEKINGSVLPFGCAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLQCAPELLG 120
Db 61 IVFPEKINGSVLPFGCAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLQCAPELLG 120
QY 121 GAEPGYLTGTINGDPESVASLHWDGALLGVYRGAEHLQPLLEGTTNSAGGPGCAHI 180
Db 121 GAEPGYLTGTINGDPESVASLHWDGALLGVYRGAEHLQPLLEGTTNSAGGPGCAHI 180
QY 181 LRRKSPASGOGPMCNVKAPLGSPSPRRRAKRFAISLRSFVETILVAVDDKMAAFHAGLKR 240
Db 181 LRRKSPASGOGPMCNVKAPLGSPSPRRRAKRFAISLRSFVETILVAVDDKMAAFHAGLKR 240
QY 241 YLLTVMAAAKAFKHSIRNPVSLVTRVLVILSGEGEPQVGSAAQTLSFCAWQGLN 300
Db 241 YLLTVMAAAKAFKHSIRNPVSLVTRVLVILSGEGEPQVGSAAQTLSFCAWQGLN 300
QY 301 TPEDSDPDHEDTALFTRODLCCGVSTCDTGMADVGVTCDPARSCAIVEDDGLQSAFTAA 360
Db 301 TPEDSDPDHEDTALFTRODLCCGVSTCDTGMADVGVTCDPARSCAIVEDDGLQSAFTAA 360
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Db 301 TPEDSGPDHFDTAILFTTRQDLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAA 360
 QY 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAVMAHVDPPEPWPSCSARFTITDFLDNGY 420
 Db 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAVMAHVDPPEPWPSCSARFTITDFLDNGY 420
 QY 421 GHCLLDKPEAPLHLVPTFGKDYADROCOLTFTGPDSDRHCPCOLPPPCAALWCSEHLNGHA 480
 Db 421 GHCLLDKPEAPLHLVPTFGKDYADROCOLTFTGPDSDRHCPCOLPPPCAALWCSEHLNGHA 480
 QY 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWPWPGDSCRTCCGGV 540
 Db 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWPWPGDSCRTCCGGV 540
 QY 541 QFSRDCTRPVPRNGKCYCEGRTRFRSCNTEDCPTGSAITFREEOCAAYNHTDLFKSF 600
 Db 541 QFSRDCTRPVPRNGKCYCEGRTRFRSCNTEDCPTGSAITFREEOCAAYNHTDLFKSF 600
 QY 601 PGPMWVPRYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSSVCVQGRCIHA 660
 Db 601 PGPMWVPRYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSSVCVQGRCIHA 660
 QY 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQOQNP 720
 Db 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQOQNP 720
 QY 721 GHRISYLAUKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAAETLSGHGFLAQP 780
 Db 721 GHRISYLAUKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAAETLSGHGFLAQP 780
 QY 781 LTLQVLVAGNQDTRLRYSFVPRPTPTPTQDMLHRRQAILEILRRRPWAGRK 837
 Db 781 LTLQVLVAGNQDTRLRYSFVPRPTPTPTQDMLHRRQAILEILRRRPWAGRK 837

RESULT 9
 AAB66178
 ID AAB66178 standard; protein; 837 AA.
 AC AAB66178;
 XX
 XX
 DT 02-APR-2001 (first entry)
 DE Protein of the invention #90.
 XX
 XX Secreted; transmembrane; gene therapy.
 OS Unidentified.
 XX
 XX WO2000/78961-A1.
 PN
 PD 28-DEC-2000.
 XX
 PF 18-FEB-2000; 2000WO-US004342.
 XX
 XX 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Cao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Fan J, Paoni NF, Roy WA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WI;
 XX

DR WPI; 2001-071395/08.
 XX Secreted and transmembrane proteins and nucleic acids designated PRO,
 PT useful as hybridization probes, in chromosome and gene mapping and gene
 PT therapy.
 XX Claim 1; Fig 180; 787pp; English.
 XX The present invention relates to secreted and transmembrane proteins.
 CC These proteins and the DNA encoding them may be used as hybridization
 CC probes, in chromosome and gene mapping and in the generation of anti-
 CC sense RNA and DNA. They may also be used to generate either
 CC transgenic animals or knockout animals which are in turn useful for
 CC development and screening of therapeutically useful reagents. The nucleic
 CC acids may also be used in gene therapy
 XX Sequence 837 AA;
 SQ

Query Match 99.8%; Score 4563; DB 4; Length 837;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSQTGSHFGRGLAGRWLWGAQPCILLPIVPLSWLWLLLLILLASLLPSARLASPLPREE 60
 Db 1 MSQTGSHFGRGLAGRWLWGAQPCILLPIVPLSWLWLLLLILLASLLPSARLASPLPREE 60
 QY 61 IVFPEKLVSVLPSSGAPARLLCRLOAFGETLLELEODSGVQVEGLTVQYLQOAPPELLG 120
 Db 61 IVFPEKLVSVLPSSGAPARLLCRLOAFGETLLELEODSGVQVEGLTVQYLQOAPPELLG 120
 QY 121 GAEPCTYLTGTINGDPESVASLHWDGGALLGVLYRGAEHLQPLEGGTPNSAGGFGAHI 180
 Db 121 GAEPCTYLTGTINGDPESVASLHWDGGALLGVLYRGAEHLQPLEGGTPNSAGGFGAHI 180
 QY 181 LRRKSPASQGGPMCNVKAPLGSPSPRRRAKFAFSLRPFVETLVVADDDKMAAFHAGLKR 240
 Db 181 LRRKSPASQGGPMCNVKAPLGSPSPRRRAKFAFSLRPFVETLVVADDDKMAAFHAGLKR 240
 QY 241 YLLTVMAAAAKAFKPSIRNPVSLVTVLVLGSGEEGPQVGPAAQTURSCAMORGLN 300
 Db 241 YLLTVMAAAAKAFKPSIRNPVSLVTVLVLGSGEEGPQVGPAAQTURSCAMORGLN 300
 QY 301 TPEDSDPDHFDTAILFTTRQDLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAA 360
 Db 301 TPEDSDPDHFDTAILFTTRQDLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAA 360
 QY 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAVMAHVDPPEPWPSCSARFTITDFLDNGY 420
 Db 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAVMAHVDPPEPWPSCSARFTITDFLDNGY 420
 QY 421 GHCLLDKPEAPLHLVPTFGKDYADROCOLTFTGPDSDRHCPCOLPPPCAALWCSEHLNGHA 480
 Db 421 GHCLLDKPEAPLHLVPTFGKDYADROCOLTFTGPDSDRHCPCOLPPPCAALWCSEHLNGHA 480
 QY 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWPWPGDSCRTCCGGV 540
 Db 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWPWPGDSCRTCCGGV 540
 QY 541 QFSRDCTRPVPRNGKCYCEGRTRFRSCNTEDCPTGSAITFREEOCAAYNHTDLFKSF 600
 Db 541 QFSRDCTRPVPRNGKCYCEGRTRFRSCNTEDCPTGSAITFREEOCAAYNHTDLFKSF 600
 QY 601 PGPMWVPRYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSSVCVQGRCIHA 660
 Db 601 PGPMWVPRYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSSVCVQGRCIHA 660
 QY 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQOQNP 720
 Db 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQOQNP 720
 QY 721 GHRISYLAUKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAAETLSGHGFLAQP 780
 Db 721 GHRISYLAUKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAAETLSGHGFLAQP 780

QY 781 LTLQVLVAGNPDQTRLYSFFVPRPTPTPQDMLHRRRAQILILRRRPWAGRK 837
DB 781 LTLQVLVAGNPDQTRLYSFFVPRPTPTPQDMLHRRRAQILILRRRPWAGRK 837

RESULT 10
AAU29199
ID AAU29199 standard; protein; 837 AA.

XX AAU29199;
XX
DT 18-DEC-2001 (first entry)
XX
XX Human PRO polypeptide sequence #176.
XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
XX Homo sapiens.
XX
XX W0200168848-A2.
XX
XX 20-SEP-2001.
XX
XX 28-FEB-2001; 2001WO-US006520.
XX
XX 01-MAR-2000; 2000WO-US005601.
XX 02-MAR-2000; 2000WO-US005841.
XX 03-MAR-2000; 2000US-0187202P.
XX 06-MAR-2000; 2000US-0186968P.
XX 14-MAR-2000; 2000US-0189320P.
XX 14-MAR-2000; 2000US-0189328P.
XX 15-MAR-2000; 2000WO-US006884.
XX 21-MAR-2000; 2000US-0190828P.
XX 21-MAR-2000; 2000US-0191007P.
XX 21-MAR-2000; 2000US-0191048P.
XX 21-MAR-2000; 2000US-0191314P.
XX 28-MAR-2000; 2000US-0192655P.
XX 29-MAR-2000; 2000US-0193032P.
XX 29-MAR-2000; 2000US-0193053P.
XX 30-MAR-2000; 2000WO-US008439.
XX 04-APR-2000; 2000US-0194449P.
XX 04-APR-2000; 2000US-0194647P.
XX 11-APR-2000; 2000US-0195975P.
XX 11-APR-2000; 2000US-0196000P.
XX 11-APR-2000; 2000US-0196187P.
XX 11-APR-2000; 2000US-0196690P.
XX 11-APR-2000; 2000US-0196820P.
XX 18-APR-2000; 2000US-0198121P.
XX 18-APR-2000; 2000US-0198585P.
XX 25-APR-2000; 2000US-0199397P.
XX 25-APR-2000; 2000US-0199550P.
XX 25-APR-2000; 2000US-0199654P.
XX 03-MAY-2000; 2000US-0201516P.
XX 17-MAY-2000; 2000WO-US013705.
XX 22-MAY-2000; 2000WO-US014042.
XX 30-MAY-2000; 2000WO-US014941.
XX 02-JUN-2000; 2000WO-US015264.
XX 05-JUN-2000; 2000US-0209832P.
XX 28-JUL-2000; 2000WO-US020710.
XX 22-AUG-2000; 2000US-0064848.
XX 24-AUG-2000; 2000WO-US023328.
XX 08-NOV-2000; 2000WO-US030952.
XX 01-DEC-2000; 2000WO-US032678.
XX 20-DEC-2000; 2000WO-US034956.
XX
XX (GETH) GENENTECH INC.
XX Baker KP, Chen J, Deanyovers L, Goddard A, Godowski PJ, Gurney AL;
XX Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

XX WPI: 2001-602746/68.
DR N-PSDB; AAS46100.
XX
PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX
PS Claim 11; Fig 352; 774pp; English.
XX
XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX
XX Sequence 837 AA;
SQ

Query Match 99.8%; Score 4563; DB 4; Length 837;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSQTGSHPCGRGLACRWLWGAQPCILLPIVPLSWLWLLLLASLLPSARLASPLPREE 60
DB 1 MSQTGSHPCGRGLACRWLWGAQPCILLPIVPLSWLWLLLLASLLPSARLASPLPREE 60
QY 61 IVFPEKLINGSVLPFGSGAPARLLCRLOAFGCTLLLELEQDSGVQVEGLTVQYLGAPELLG 120
DB 61 IVFPEKLINGSVLPFGSGAPARLLCRLOAFGCTLLLELEQDSGVQVEGLTVQYLGAPELLG 120
QY 121 GAEPGYLTGTINGDPDESVAHLWDGALLGVLYRGAELHLOPLEGGTNSAGGGAHI 180
DB 121 GAEPGYLTGTINGDPDESVAHLWDGALLGVLYRGAELHLOPLEGGTNSAGGGAHI 180
QY 181 LRRKSPASGCGPMCNVKAPLGSPSPRPRAKFASLSRFRVETLVVADDKMAAFHGLAKR 240
DB 181 LRRKSPASGCGPMCNVKAPLGSPSPRPRAKFASLSRFRVETLVVADDKMAAFHGLAKR 240
QY 241 YLLTVMAAAKAFKHPISIRNPVSLVTRVLVILSGEGEPQVGPSSAQTLSFCWQKGLN 300
DB 241 YLLTVMAAAKAFKHPISIRNPVSLVTRVLVILSGEGEPQVGPSSAQTLSFCWQKGLN 300
QY 301 TPEDSDPDHFDTAILFTRODLGCVSTCDTLGMADVGTCDPARSCAIVEDDGLQSAFTAA 360
DB 301 TPEDSDPDHFDTAILFTRODLGCVSTCDTLGMADVGTCDPARSCAIVEDDGLQSAFTAA 360
QY 361 HELGHVFNMLHDNSKPCISLNGPLSTRHVMAVMAHVDPEEPWSPCSARFIFDLDNGY 420
DB 361 HELGHVFNMLHDNSKPCISLNGPLSTRHVMAVMAHVDPEEPWSPCSARFIFDLDNGY 420
QY 421 GHCLLDKPEAPLHPVTFFPKDYADRCQLTGPDSRHCPQLPPPPCAALWCSGHLNGHA 480
DB 421 GHCLLDKPEAPLHPVTFFPKDYADRCQLTGPDSRHCPQLPPPPCAALWCSGHLNGHA 480
QY 481 MCOTKSPWADGTPCGPAQACMGRCILHMDLODENIPOAGGKWPMPGWCDCSRTCGGV 540
DB 481 MCOTKSPWADGTPCGPAQACMGRCILHMDLODENIPOAGGKWPMPGWCDCSRTCGGV 540
QY 541 QFSRDCTRPVPRNGKYCEGRTRFRSCNTECDPTGSGALTFFREEQCAAYNHRITDLFKSF 600
DB 541 QFSRDCTRPVPRNGKYCEGRTRFRSCNTECDPTGSGALTFFREEQCAAYNHRITDLFKSF 600

QY 601 PGMWVPRYTGVAPOQCKLTQCARALGYVYVLEPRVVDGTPCSPDSSVCVQGRCIHA 660
DB 601 PGMWVPRYTGVAPOQCKLTQCARALGYVYVLEPRVVDGTPCSPDSSVCVQGRCIHA 660
QY 661 GCDRIIGSKKPKDKWCCGDSGCKSQSGSKPKFRYGVNNVTIPAGATHILVROQGNP 720
DB 661 GCDRIIGSKKPKDKWCCGDSGCKSQSGSKPKFRYGVNNVTIPAGATHILVROQGNP 720
QY 721 GHRSIYLALKPDGSLANGEXTLMPSPDVLPGAVSLRYSGATAASETLSGHGFLAOP 780
DB 721 GHRSIYLALKPDGSLANGEXTLMPSPDVLPGAVSLRYSGATAASETLSGHGFLAOP 780
QY 781 LTIQVLVAGNPQDTRLRYSFVPRPTSPRPPQDMLHRRQAQILRLRRPWAGRK 837
DB 781 LTIQVLVAGNPQDTRLRYSFVPRPTSPRPPQDMLHRRQAQILRLRRPWAGRK 837

RESULT 11
ABUS8575
ID ABUS8575 standard; protein; 837 AA.
AC ABUS8575;
XX
DT 15-APR-2003 (first entry)
XX
DE Human PRO polypeptide #176.
KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEFT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
XX OS Homo sapiens.
XX
XX PN
XX PD US2003027272-A1.
XX
XX PF 06-FEB-2003.
XX
XX 21-JUN-2002; 2002US-00176492.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
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PR 11-DEC-1997; 97US-0069335P.
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PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
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PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.

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PR	26-JUN-1998;	98US-00105413.	Query Match	99.8%;	Score 4563;	DB 6;	Length 837;
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PR	06-OCT-1998;	98US-0103258P.					
PR	06-OCT-1998;	98US-0103449P.					
PR	07-OCT-1998;	98US-00168978.					
QY	1	MSQTGSHEGRGLAGRWLWGAQPCLLLPVPLSWLWVLLLLLSALLPSARLASLPREEE	60				
DB	1	MSQTGSHEGRGLAGRWLWGAQPCLLLPVPLSWLWVLLLLLSALLPSARLASLPREEE	60				
QY	61	IVFPEKLVPGSGAPARLLCHLOARGETLLELEODSGVOVEGLTVQVYLGAPPELLG	120				
DB	61	IVFPEKLVPGSGAPARLLCHLOARGETLLELEODSGVOVEGLTVQVYLGAPPELLG	120				
QY	121	GAEPGTILTGTINGDPESVASLHWDGGALLGVLYRGAEHLHLPLEGCTPNSAGPGGAIH	180				
DB	121	GAEPGTILTGTINGDPESVASLHWDGGALLGVLYRGAEHLHLPLEGCTPNSAGPGGAIH	180				
QY	181	LRKSPASGQGMVNCVKAFLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKR	240				
DB	181	LRKSPASGQGMVNCVKAFLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKR	240				
QY	241	YLLTWAAAAAKAFKHPSTRNPVSLVTVTLVILGSGEGPOVGPSSAAQTLRSCAWORGLN	300				
DB	241	YLLTWAAAAAKAFKHPSTRNPVSLVTVTLVILGSGEGPOVGPSSAAQTLRSCAWORGLN	300				
QY	301	TPEDSDPDHFDTAILFTTRQDLGCVSTCDTLGMADYGTVCDPARSCAIVEDDGLQSAFTAA	360				
DB	301	TPEDSDPDHFDTAILFTTRQDLGCVSTCDTLGMADYGTVCDPARSCAIVEDDGLQSAFTAA	360				
QY	361	HELGHVFNMLHDNSKPCISLNGPLSTSRHVMAVMAHVDPPEPWPSPCSARFTDLDNGY	420				
DB	361	HELGHVFNMLHDNSKPCISLNGPLSTSRHVMAVMAHVDPPEPWPSPCSARFTDLDNGY	420				
QY	421	GHCLLDKPEAPLHLPVTFPGDYDADROCOLTFGPDSPHCPOLPPPCALWCSGHLNGHA	480				
DB	421	GHCLLDKPEAPLHLPVTFPGDYDADROCOLTFGPDSPHCPOLPPPCALWCSGHLNGHA	480				
QY	481	MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWPWPGWDCSRTCCGGV	540				
DB	481	MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWPWPGWDCSRTCCGGV	540				
QY	541	QFSRDCTRPVPRNGKCYCEGRTRFRSCNTDCTGSAITFREOCAYNHTDLFKSF	600				
DB	541	QFSRDCTRPVPRNGKCYCEGRTRFRSCNTDCTGSAITFREOCAYNHTDLFKSF	600				
QY	601	PGMDWVPRTYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSSVCVQGRCIHA	660				
DB	601	PGMDWVPRTYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSSVCVQGRCIHA	660				
QY	661	GCDRIIGSKKFKDKMVCVCGDGGSCSKQSGSPRFRKYGYNNVVTIPAGATHILVROQGNP	720				
DB	661	GCDRIIGSKKFKDKMVCVCGDGGSCSKQSGSPRFRKYGYNNVVTIPAGATHILVROQGNP	720				
QY	721	GHRSIYIALKLPDGSVALNGEYTLMPSTDDVLPAGAVSLRYSGATAASTLSHGGLAQP	780				
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QY	781	LTLQVLVAGNPQDTRLYRFFVPRPTPTPQDHLHRRQAQILRILRRRPMWAGRK	837				
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XX	AC	ABU88123;					
XX	DT	07-JUL-2003 (first entry)					
XX	DE	Novel human secreted and transmembrane protein PRO1563.					
XX	KW	Human; secreted and transmembrane protein: PRO; gene therapy;					

KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
XX prostate tumour; rectal tumour; cervical tumour; liver tumour.

OS Homo sapiens.
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XX US2003032127-A1.
XX 13-FEB-2003.
XX 26-JUN-2002; 2002US-00183012.
XX 18-SEP-1997; 97US-0059263P.
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Qy	361	HELGHVFNMLHDSKPCISLNGPLSTSRHVMAFVMAHVDPEEPWPCSA	420	PR	28-OCT-1997; 97US-0063540P.
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Qy	421	GHCLLDKPEAPLHLPVTFFPKGYDADRCOLTFGPDSPHCPOLPPCAALM	480	PR	28-OCT-1997; 97US-0063544P.
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Qy	541	QFSRSDCTRPVPRNGKCYCBGRTRFRSCNTEDCPTGSALTFRBEOCAA	600	PR	31-OCT-1997; 97US-0064103P.
Db	541	QFSRSDCTRPVPRNGKCYCBGRTRFRSCNTEDCPTGSALTFRBEOCAA	600	PR	97US-0065311P.
Qy	601	PGMDWVPRTYGVAPQDCKLTQARALGYVYVLEPRVVDGTFCSPDSSVC	660	PR	21-NOV-1997; 97US-0066120P.
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Qy	721	GHRISYIALKLPDGSYALNGEYTLMPSTDVLPGLVSLRYSGATASETLS	780	PR	11-DEC-1997; 97US-0069425P.
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Qy	781	LTLQVLVAGNPQDTRLRYSFVPRPTSTPRPTQDMLHRAQILEILRRR	837	PR	17-DEC-1997; 97US-0068017P.
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XX	ABR65702;				98US-0078939P.
AC	ABR65702;				98US-0079664P.
XX	05-AUG-2003 (first entry)				98US-0079786P.
DT	Human secreted polypeptide PRO1563, SEQ ID NO:352.				98US-0080107P.
DE	Human; PRO; secreted protein; transmembrane protein;				98US-0080194P.
XX	extracellular domain; tumour necrosis factor-alpha; TNF-alpha;				98US-0080322P.
KW	chondrocyte; proliferation; differentiation; cartilage disorder;				98US-0080333P.
KW	bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;				98US-0081049P.
KW	adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;				98US-0081070P.
KW	liver; drug screening; transgenic animal; genetic analysis;				98US-0081195P.
XX	antiarthritic; vulnery; gene therapy.				98US-0081838P.
OS	Homo sapiens.				98US-0082568P.
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PR	25-JUN-1998;	98US-0090676P.	PR	30-SEP-1998;	98US-0102571P.
PR	25-JUN-1998;	98US-0090688P.	PR	01-OCT-1998;	98US-0102684P.
PR	25-JUN-1998;	98US-0090690P.	PR	01-OCT-1998;	98US-0102687P.
PR	25-JUN-1998;	98US-0090694P.	Query Match 99.8%; Score 4563; DB 6; Length 837;		
PR	25-JUN-1998;	98US-0090695P.	Best Local Similarity 99.9%; Pred. No. 0;		
PR	25-JUN-1998;	98US-0090696P.	Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
PR	26-JUN-1998;	98US-00105413.	Qy	1	MSQTGSHPGRGLAGRLMGAQPCLLLPVPLSLVWLWLLLLASLLPSARLASPLPREE 60
PR	26-JUN-1998;	98US-0090862P.	Db	1	MSQTGSHPGRGLAGRLMGAQPCLLLPVPLSLVWLWLLLLASLLPSARLASPLPREE 60
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PR	26-JUN-1998;	98US-0091010P.	Db	61	IVFPEKLVGSLPGSGAPARLLCRLLQAFGETLLLEQDSGVQVEGLTVQYLQAPPELLG 120
PR	01-JUL-1998;	98US-0091359P.	Qy	121	GAEPGTTLTGTTINGDPESVASLHWGGALLGVLYRGAELHLQPLEGGTNSAGGPGAH 180
PR	01-JUL-1998;	98US-0091544P.	Db	121	GAEPGTTLTGTTINGDPESVASLHWGGALLGVLYRGAELHLQPLEGGTNSAGGPGAH 180
PR	02-JUL-1998;	98US-0091478P.	Qy	181	LRRKSPASGQGMVNCVAPLGSPPRRRAKRFASI-SRFVETLVVADDKMAAFHAGLKR 240
PR	02-JUL-1998;	98US-0091626P.	Db	181	LRRKSPASGQGMVNCVAPLGSPPRRRAKRFASI-SRFVETLVVADDKMAAFHAGLKR 240
PR	02-JUL-1998;	98US-0091628P.	Qy	241	YLLTWAAAAAFKHPSIRNPVSLVTRVLVILSGSEEGPQVGPSPAAQTLSFCAWORGLN 300
PR	02-JUL-1998;	98US-0091632P.	Db	241	YLLTWAAAAAFKHPSIRNPVSLVTRVLVILSGSEEGPQVGPSPAAQTLSFCAWORGLN 300
PR	04-AUG-1998;	98US-0094006P.	Qy	301	TPEDSDPDHFDTAILFTTRQDLCGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAA 360
PR	10-AUG-1998;	98US-0095998P.	Db	301	TPEDSDPDHFDTAILFTTRQDLCGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAA 360
PR	10-AUG-1998;	98US-0096012P.	Qy	361	HELGHVFNWMLHDNSKPCISLNGPLSTSRHVMAVMAHVDPEEPWSPCSARFITDFLDNGY 420
PR	17-AUG-1998;	98US-0096766P.	Db	361	HELGHVFNWMLHDNSKPCISLNGPLSTSRHVMAVMAHVDPEEPWSPCSARFITDFLDNGY 420
PR	17-AUG-1998;	98US-0096867P.	Qy	421	GHCLLDKPEAPLHLPVTFPGKDYDADRCQLTFFGPDNRHCPQLPPPCAAALWCSHGLNGHA 480
PR	17-AUG-1998;	98US-0096891P.	Db	421	GHCLLDKPEAPLHLPVTFPGKDYDADRCQLTFFGPDNRHCPQLPPPCAAALWCSHGLNGHA 480
PR	17-AUG-1998;	98US-0096897P.	Qy	481	MCQTKHSPWADGTPCGPAQACMGGRCLHMDQLQDNFIPOAGGWMGPMGDCSRTCCGVV 540
PR	18-AUG-1998;	98US-0096949P.	Db		
PR	18-AUG-1998;	98US-0096959P.			
PR	18-AUG-1998;	98US-0097022P.			
PR	26-AUG-1998;	98US-0097952P.			
PR	26-AUG-1998;	98US-0097954P.			
PR	26-AUG-1998;	98US-0097955P.			
PR	26-AUG-1998;	98US-0097971P.			
PR	26-AUG-1998;	98US-0097974P.			
PR	01-SEP-1998;	98US-0098014P.			
PR	01-SEP-1998;	98US-0098716P.			
PR	01-SEP-1998;	98US-0098723P.			
PR	02-SEP-1998;	98US-0098803P.			
PR	02-SEP-1998;	98US-0098821P.			
PR	02-SEP-1998;	98US-0098843P.			
PR	09-SEP-1998;	98US-0099602P.			

Fri Apr 1 15:02:39 2005

us-09-634-287e-2.rag

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Db	541	QFSSRDCTRPVPRNGGKYCEGRTRFRSCNTEDCPTGSALTFRERQCAAYNHRTDLFKSF	600
Qy	601	PGFMDVPRYTGVAPQDQCKLTCQARALGYVYVLEPRVVDGTPCSPDSSSVCVQGRCIHA	660
Db	601	PGFMDVPRYTGVAPQDQCKLTCQARALGYVYVLEPRVVDGTPCSPDSSSVCVQGRCIHA	660
Qy	661	GCDRIIGSKKKFKDKMVCQDGGSCSKSGSRKFRYGYNNVVTIPAGATHILVRQGNP	720
Db	661	GCDRIIGSKKKFKDKMVCQDGGSCSKSGSRKFRYGYNNVVTIPAGATHILVRQGNP	720
Qy	721	GHSIYILALKLPDGSVALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSGHGFLAQP	780
Db	721	GHSIYILALKLPDGSVALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSGHGFLAQP	780
Qy	781	LTLQVLVAGNPQDTRLRYSPFVPRPTSTPRTPQDMLHRAQILEILRRPWAGRK	837
Db	781	LTLQVLVAGNPQDTRLRYSPFVPRPTSTPRTPQDMLHRAQILEILRRPWAGRK	837

Search completed: April 1, 2005, 12:48:26
Job time : 186 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 12:21:01 ; Search time 43 Seconds
(without alignments)
1453.053 Million cell updates/sec

Title: US-09-634-287E-2

Perfect score: 4570

Sequence: 1 MSQTSHPGRLAGRWLGA.....LHRAQILEILRRRPWAGR 837

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
 - 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
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 - 4: /cgn2_6/prodata/1/iaa/6B_COMB.pep:*
 - 5: /cgn2_6/prodata/1/iaa/PCUS_COMB.pep:*
 - 6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4570	100.0	837	4	US-09-122-126B-2
2	4570	100.0	837	4	US-09-634-286A-2
3	4570	100.0	837	4	US-10-247-685-2
4	2158	47.2	950	4	US-09-321-987B-4
5	2135	46.7	967	4	US-09-130-491-2
6	2131	46.6	949	4	US-09-568-559-2
7	1998.5	43.7	727	4	US-09-445-023A-1
8	1986	43.5	727	4	US-09-445-023A-12
9	1917	41.9	950	3	US-10-009-332-1
10	1824	39.9	905	3	US-09-369-364A-9
11	1793.5	39.2	608	4	US-09-130-491-13
12	1576	34.5	930	3	US-09-369-364A-2
13	1558	34.1	930	4	US-09-122-126B-15
14	1558	34.1	930	4	US-09-634-286A-15
15	1558	34.1	930	4	US-10-247-685-15
16	1456	31.9	1882	3	US-09-369-364A-13
17	1380.5	30.2	874	3	US-09-369-364A-15
18	1368.5	29.9	551	4	US-09-130-491-16
19	1327.5	29.0	2150	4	US-09-321-987B-2
20	1317	28.8	2165	4	US-09-800-729-155
21	1172	25.6	908	4	US-09-963-791-2
22	1139.5	24.9	757	4	US-09-963-791-24
23	1105.5	24.2	1104	4	US-09-981-953A-4
24	1086	23.8	481	4	US-09-130-491-8
25	1059	23.2	518	3	US-09-369-364A-22
26	1043	22.8	997	3	US-09-369-364A-7
27	982	21.5	859	3	US-09-369-364A-5

28	975	21.3	1224	4	US-09-930-872-4	Sequence 4, Appli
29	975	21.3	1224	4	US-10-217-774-4	Sequence 4, Appli
30	973.5	21.3	1081	3	US-09-369-364A-17	Sequence 17, Appl
31	953.5	20.9	1211	4	US-09-949-016-11401	Sequence 11401, A
32	950.5	20.8	969	4	US-09-321-987B-5	Sequence 5, Appli
33	935.5	20.5	1211	4	US-09-491-522-5	Sequence 11, Appl
34	920.5	20.1	1205	4	US-09-491-522-11	Sequence 2, Appli
35	858.5	18.8	770	4	US-09-981-953A-2	Sequence 7859, Ap
36	725	15.9	1039	4	US-09-949-016-7859	Sequence 12, Appl
37	710	15.5	589	4	US-09-963-791-12	Sequence 22, Appl
38	677.5	14.8	438	4	US-09-963-791-22	Sequence 11, Appl
39	639	14.0	245	3	US-09-369-364A-11	Sequence 10, Appl
40	547.5	12.0	507	4	US-09-963-791-10	Sequence 20, Appl
41	515	11.3	356	4	US-09-963-791-20	Sequence 7, Appli
42	475.5	10.4	566	4	US-09-491-522-7	Sequence 7010, Ap
43	471.5	10.3	566	4	US-09-949-016-7010	Sequence 8505, Ap
44	471.5	10.3	566	4	US-09-949-016-8505	Sequence 6, Appli
45	454	9.9	468	4	US-09-963-791-6	

ALIGNMENTS

RESULT 1

US-09-122-126B-2
; Sequence 2, Application US/09122126B
; Patent No. 6451575
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGREGAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909
; CURRENT APPLICATION NUMBER: US/09/122,126B
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-122-126B-2

Query Match 100.0%; Score 4570; DB 4; Length 837;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 837; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	IVFPEKLINGSVLPGSGAPARLLCRLOAQFGETLLLEQDSGVQVEGLTVQYLQAPPELLG	120
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Qy	121	GAEPGYLTGTINGDPESVASLHWDGALLGVLYRGAEHLQPLEGGTPNSAGGFGAHI	180
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Qy	181	LRRKPSAQGGPWCNVKAPLGSPSPRRPRAKFPASLSRFVETLVVADDDKMAAFHAGLKR	240
Db	181	LRRKPSAQGGPWCNVKAPLGSPSPRRPRAKFPASLSRFVETLVVADDDKMAAFHAGLKR	240
Qy	241	YLLTWMAAAKAFKHPISRNPNVSLVTRVLVILGSGEGPQVGPSPAAQTILRSFCAMORGLN	300
Db	241	YLLTWMAAAKAFKHPISRNPNVSLVTRVLVILGSGEGPQVGPSPAAQTILRSFCAMORGLN	300
Qy	301	TPEDSDPHDFTAILFTTRQDLGCVSTCDTLGMADVTGTCDPARSCAIVEDDDGLQSAFTAA	360
Db	301	TPEDSDPHDFTAILFTTRQDLGCVSTCDTLGMADVTGTCDPARSCAIVEDDDGLQSAFTAA	360
Qy	361	HELGHVFNMLHDNSKPCISLNGPLSTSRHVMAVMAHVDPEEPWSPCSARFTITDFLDNGY	420
Db	361	HELGHVFNMLHDNSKPCISLNGPLSTSRHVMAVMAHVDPEEPWSPCSARFTITDFLDNGY	420


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QY 241 YLTVMAAAKAFKPSIRNPVSLVTRVLVILSGEGPQVPSAAQTLSFCAWQGLN 300
DB 241 YLTVMAAAKAFKPSIRNPVSLVTRVLVILSGEGPQVPSAAQTLSFCAWQGLN 300
QY 301 TPEDSDPDHFDTAILFTRODLGVSTCDTILGMADVGVTCVCDPARSCAIVEDDGLQSAFTAA 360
DB 301 TPEDSDPDHFDTAILFTRODLGVSTCDTILGMADVGVTCVCDPARSCAIVEDDGLQSAFTAA 360
QY 361 HELGHVFNMLHDSKPCISLNGPLSTRHVMAPVMAHVDPEEPWSPCSARFIITDFLDNGY 420
DB 361 HELGHVFNMLHDSKPCISLNGPLSTRHVMAPVMAHVDPEEPWSPCSARFIITDFLDNGY 420
QY 421 GHCLLDKPEAPLHLPVTFPGKYDADRQCLTFCGDSRHCQPLPPPCAAALWCSGHLNGHA 480
DB 421 GHCLLDKPEAPLHLPVTFPGKYDADRQCLTFCGDSRHCQPLPPPCAAALWCSGHLNGHA 480
QY 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDLODFNIPOAGGNGPWPWGDCSRTCCGGV 540
DB 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDLODFNIPOAGGNGPWPWGDCSRTCCGGV 540
QY 541 QFSRDCTRPVPRNGGKYCEGRTRFRSCNTEDCPTGSALTFRBEOCAAYNHRTDLFKSF 600
DB 541 QFSRDCTRPVPRNGGKYCEGRTRFRSCNTEDCPTGSALTFRBEOCAAYNHRTDLFKSF 600
QY 601 PGPMWVRYTGVAPQDQCKLTQCARALGYVYVLEPRVVDGTPCSPDSSVCVQGRCIHA 660
DB 601 PGPMWVRYTGVAPQDQCKLTQCARALGYVYVLEPRVVDGTPCSPDSSVCVQGRCIHA 660
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DB 661 GCDRIIGSKKFKDKMVCVCGDGGSCSKSGSPKFRFYGYNNVTIIPAGATHILVROQGNP 720
QY 721 GHRISYIALKLPDGSVALNGEYTLMPSTDVLPGLAVSLRYSGATASSETLSHGGLAOP 780
DB 721 GHRISYIALKLPDGSVALNGEYTLMPSTDVLPGLAVSLRYSGATASSETLSHGGLAOP 780
QY 781 LTLQVLVAGNPQDTRLRYSFVFPRTPTSTPRTPQDMLHRAQILBILRRRPWAGR 837
DB 781 LTLQVLVAGNPQDTRLRYSFVFPRTPTSTPRTPQDMLHRAQILBILRRRPWAGR 837

RESULT 4
US-09-321-987B-4
; Sequence 4, Application US/09321987B
; Patent No. 6730820
; GENERAL INFORMATION:
; APPLICANT: Kimble, Judith E
; APPLICANT: Bielloch, Robert H
; TITLE OF INVENTION: Agent and Method for Modulating Cell Migration
; FILE REFERENCE: 960296.95386
; CURRENT APPLICATION NUMBER: US/09/321,987B
; CURRENT FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,170
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/129,023
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 950
; TYPE: PRT
; ORGANISM: Murine
US-09-321-987B-4

Query Match 47.2%; Score 2158; DB 4; Length 950;
Best Local Similarity 49.4%; Pred. No. 2.9e-154;
Matches 414; Conservative 135; Mismatches 221; Indels 68; Gaps 16;

QY 37 LMLLLAS--LPSARIA--SPLPREEEIVFPEKINGSVLPGSGAPARLLCRILQAFGETL 92
DB 18 LMLLLASITMLLCAGAGRPTDEELVPSLERA---PGHDSITTRL-RUDAFGOQL 73
QY 93 LLEEQDSGVQVEGLTVQVILGAPELLGGAE-----PGTYLTGTINGDPESVASL 142
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DB 74 HLKLPDQSGFLAPGFTLQTVGRSP-----GSEAQHLDPTGLAHCFYSGTVNGDPGSAAL 129
QY 143 HWDGGALLGVQVRGAELHLQPLEG-----GTP--NSAGGPGAHILRRKSPASQGP 192
DB 130 SLCEG--VRGAFYLGQEEFFIQPAPVATERLAPVPEESSARPQPHILRRRGSG-GA 187
QY 193 MCNV-----KAPLAGSPSPRR-----RAKRPFASLSRFVETL 223
DB 188 KCGWMDDELTPSDSRPESQNTENQVDPDTPQDACKSPGSGIRKFRVSPRYVETM 247
QY 224 VVADDKMAAFHAGLKYLLTVMAAAKAFKPSIRNPVSLVTRVLVILSGEGPQVGP 283
DB 248 LVADQSMADPHSGSLKHYLLTFSAARFYKPSIRNSISLVVVKILVIEEQKGPVTS 307
QY 284 SRAQTLSRCAMQRGINTPDSDPDHFDTAILFTRODLGVSTCDTILGMADVGVTCVCDPAR 343
DB 308 NAALTURNFCNMWQKNSPSDRPEHYDTAILFTRODLGVSTCDTILGMADVGVTCVCDPSR 367
QY 344 SCAIVEDDGLQSAFTAHAHELGHVFNMLHDSKPCISLNGPLSTRHVMAPVMAHVDPEEP 403
DB 368 SCSEIEDDGLQAAFTTAHELGHVFNMPHDDAKHCASLNGVTGDS--HLMASMLSSLDHSQP 426
QY 404 WSPCSARFIITDFLDNGYGHCLLDKPEAPLHLPVTFPGKYDADRQCLTFCGDSRHCQPL 463
DB 427 WSPCSAYMVTSLFDNGHGECLMDKPNPIKLPDLPTGLTYDANRQCOFTFGEESKHCPDA 486
QY 464 PPCCALWCSGHLNGHAMQCTKHSWADGTPCGPAQACMGRCCLHMDLODFNIPOAGGW 523
DB 487 ASTCTTLWCTGTGGLLVLCQTRHFPWADGTSCEGKWCVSKCNKTMKHFATPVHGSW 546
QY 524 GPMGPWGDSCRTCGGVQFSSRDCTRPVPRNGGKYCEGRTRFRSCNTEDCPTGSALTFR 583
DB 547 GPMGPWGDSCRTCGGVQVYTMRECDNPVPGNGKYCEGRVRYRSCNIEDCPDNGKTFR 606
QY 584 EQCAAAYNHRTDLFKSPGPMWVRYTGVAPQDQCKLTQCARALGYVYVLEPRVVDGTP 643
DB 607 EQCEAHNBFSAKSGFNEPTVEMTPKYAGVSPKDRCKLTCEAKGIGYFFVLQPKVVDGTP 666
QY 644 CSPDSSVCVQGRCIHAGCDRIIGSKKFKDKMVCVCGDGGSCSKSGSPKFRFYGYNNV 703
DB 667 CSPDSTSVCVQGCVKAGCDRIIGSKKFKDKVCGGNGSTCKKMSGIVTSTPGYHDIV 726
QY 704 TTPAGATHILVROQGNPGRHS--IYLALKLPDGSVALNGEYTLMPSTDVLPGLAVSLRY 761
DB 727 TTPAGATHILVROQGNPGRHS--IYLALKLPDGSVALNGEYTLMPSTDVLPGLAVSLRY 785
QY 762 SGATASETLSHGGLAQLTLQVLVAGNPQDTRLRYSFVFPRTPTSTPRTPQDML 818
DB 786 SGSSAALIRIRSPSLKEPLTIQVLMVGHALRPKIKFTYFMKKKTSFNAIPTFSEWV 843

RESULT 5
US-09-130-491-2
; Sequence 2, Application US/09130491
; Patent No. 6416974
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
; FILE REFERENCE: 09404/041001
; CURRENT APPLICATION NUMBER: US/09/130,491
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: US 60/058,108
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: US 60/054,961
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-130-491-2

Query Match 46.7%; Score 2135; DB 4; Length 967;
 Best Local Similarity 49.3%; Pred. No. 1.6e-152;
 Matches 415; Conservative 127; Mismatches 226; Indels 70; Gaps 18;

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 DB 36 LLLLLAAALLAVSDALGRPSEBDEELVPELERA---PGHGT-TRL--RLHAFDQQLDLEL 89

QY 97 EQDSGVQVGLTVQYLQAPPELLGGAB---PGT-----YLTGTINGDPSPVASLHWDGGA 148
 DB 90 RPDSSFLAPGFTLQNVGRK-----SGSETPLPETDLAHCFYSGTVNGDPSSAAALSCEG- 144

QY 149 LLGVLYRGAELHLQLEGGTPNSA--GGPGA-----HILRRK----- 184
 DB 145 VRGAFYLLGEAYFIQPLPAASERLATAAPEKPPAPLQFHLRLNRQGDVGGTCGVVDDE 204

QY 185 -----SPASQGGPMCNVKA---LGSPSPRRP--RAKRFASLSRFFVETILV 224
 DB 205 PRPTGKAETEDDEGTEGEDEGQWSPQDPALQGVQPTGTGSIKKRFVSSHRYVETML 264

QY 225 VADDKMAAFHAGLKRLLYLLTVMAAAAKAFKPSIRNPVSLVTRVLVILSGSEEGPQVGPS 284
 DB 265 VADQSMAEFHGSLKHLLTLFSAARLYKHPISIRNSVLVVKILLVIHDEQKGPVTSN 324

QY 285 AAGTIRSFCAWQRIANTPDSDDPHEDTALLFTRODLGVSTCDTILGMADVGTVCDPARS 344
 DB 325 AALLTLRFNCWQKHNPSPDRDAEHYDTALLFTRODLGSGTQCDTILGMADVGTVCDPARS 384

QY 345 CAIVEDDGLQSAFTAHELGHVFNMLHNSKPCISLNGPLSTRSHVMAVPMMAHVDPEEPW 404
 DB 385 CSVIEDDGLQAAFTTAHELGHVFNMPHDDAKQCASLNG--VNQDSHMAWSMLNLSHPW 443

QY 405 SPCSARFIDTDLNGYCHLLDKPEAPLHLPTVFPKQYDADQCCQLTFFGDSRHCPQLP 464
 DB 444 SPCSAYMITSFLDNGHGECLMDKPNQPIQLPGLPGTSYDANRQCQFTFGEDSKHCPDAA 503

QY 465 PPCAALWCSHNLGHAMCOTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNTPQAGGWG 524
 DB 504 STCSTLWCTGTSGLVLCQTKHFPWADGTSCEGKWCINGKCNKTRDRHFDTPFHGSMG 563

QY 525 PMGPWDCSRTCCGGVQVQFSRDCTRPVPRNGKGYCEGRRTRFRSNTDCTPGSALTFR 584
 DB 564 MWGPWDCSRTCCGGVQVQVYTWRECDNVPKNGKGYCEGKRVYRSCNLEDCEPDNNGKTFE 623

QY 585 EQCAAYNHRDIL-FKSPFGPMWVPRYTGVAPODCKLTQCARALGYVYVLEPRVDGTP 643
 DB 624 EQCEAHNEFSKASFGSGPA--VEMIPKYAGVSPKDRCKLIQCAKIGIGYFFVLQPKVVDGTP 682

QY 644 CSPDSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGDGGSGCSKQSGSPKFRFYGNVNV 703
 DB 683 CSPDSTSVQVQGVQVAGCDRIIDSXKKFDKCGVCGGNGSTCKKISGVSPTSAPGVHDI 742

QY 704 TIPAGATHILVROQGNPHRS--IYLALKLPDGSYALNGEYTLMPSPDVLVPCAVSLRY 761
 DB 743 TIPTGATNIEVKQRNGSRNNGSFLAKAADGTIYILNGDYTLSTLEQDIMYKGV--LRY 801

QY 762 SGATASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSPFVPRTPS--TPRPTPDQWL 818
 DB 802 SGSSAALERIRSFPLKEPLTIQVLTVGNALRPKIKYTFVVKKSGSFNAIPTFSAWV 859

RESULT 6

US-09-568-559-2
 ; Sequence 2, Application US/09568559
 ; Patent No. 6649377
 ; GENERAL INFORMATION:
 ; APPLICANT: Klonowski, Paul
 ; APPLICANT: Allard, John
 ; APPLICANT: Heller, Renu
 ; APPLICANT: Van Wart, Harold
 ; TITLE OF INVENTION: Human Aggrecanase and Nucleic Acid

; TITLE OF INVENTION: Compositions Encoding the Same
 ; FILE REFERENCE: ROCH-002
 ; CURRENT APPLICATION NUMBER: US/09/568,559
 ; CURRENT FILING DATE: 2000-05-09
 ; PRIOR APPLICATION NUMBER: 60/133,343
 ; PRIOR FILING DATE: 1999-05-10
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 949
 ; TYPE: PRT
 ; ORGANISM: human
 ; US-09-568-559-2

Query Match 46.6%; Score 2131; DB 4; Length 949;
 Best Local Similarity 49.3%; Pred. No. 3.2e-152;
 Matches 416; Conservative 121; Mismatches 226; Indels 80; Gaps 18;

QY 37 LLLLLLASLLPSARLASPLPREBEEIVFPEKLGSLVLPGSGAPARLLCRLOAFQGETILLEL 96
 DB 18 LLLLLAAALLAVSDALGRPSEBDEELVPELERA---PGHGT-TRL--RLHAFDQQLDLEL 71

QY 97 EQDSGVQVGLTVQYLQAPPELLGGAB---PGT-----YLTGTINGDPSPVASLHWDGGA 148
 DB 72 RPDSSFLAPGFTLQNVGRK-----SGSETPLPETDLAHCFYSGTVNGDPSSAAALSCEG- 126

QY 149 LLGVLYRGAELHLQLEGGTPNSA--GGPGA-----HILRRKSPASQGGPMCNVKA 199
 DB 127 VRGAFYLLGEAYFIQPLPAASERLATAAPEKPPAPLQFHLRLNRQGD--VGTCGVV-- 183

QY 200 LGSPSPRRP-----DDEPRPTGKAETEDDEGTEGEDEGSAQWSPQDPALQGVQPTGTGSIKKRFVSSHRY 219
 DB 184 --DDEPRPTGKAETEDDEGTEGEDEGSAQWSPQDPALQGVQPTGTGSIKKRFVSSHRY 241

QY 220 VETLVVADDKMAAFHAGLKRLLYLLTVMAAAAKAFKPSIRNPVSLVTRVLVILSGSEEGP 279
 DB 242 VETMLVADQSMAEFHGSLKHLLTLFSAARLYKHPISIRNSVLVVKILLVIHDEQKGP 301

QY 280 QVGPSSAAQTLRSFCWQRIANTPDSDDPHEDTALLFTRODLGVSTCDTILGMADVGTVC 339
 DB 302 EVTSNAALTLRFNCWQKHNPSPDRDAEHYDTALLFTRODLGSGTQCDTILGMADVGTVC 361

QY 340 DPARSCAIYVEDDGLQSAFTAHELGHVFNMLHNSKPCISLNGPLSTRSHVMAVPMMAHVD 399
 DB 362 DESRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKQCASLNG--VNQDSHMAWSMLNLD 420

QY 400 PREPWSFCARFIDTDLNGYCHLLDKPEAPLHLPTVFPKQYDADQCCQLTFFGDSRH 459
 DB 421 HSQPMWSPCSAYMITSFLDNGHGECLMDKPNQPIQLPGLPGTSYDANRQCQFTFGEDSKH 480

QY 460 CPQLPPPCAALWCSHNLGHAMCOTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPQ 519
 DB 481 CPDAASTCTLWCTGTSGLVLCQTKHFPWADGTSCEGKWCINGKCNKTRDRHFDTPFH 540

QY 520 AGGWGPWGPWDCSRTCCGGVQVQFSRDCTRPVPRNGKGYCEGRRTRFRSNTDCTPGSA 579
 DB 541 HGSWMGMPWGPWDCSRTCCGGVQVQVYTWRECDNVPKNGKGYCEGKRVYRSCNLEDCEPDNNG 600

QY 580 LTPREQCAAYNHRDIL-FKSPFGPMWVPRYTGVAPODCKLTQCARALGYVYVLEPRV 638
 DB 601 KTFPREQCEAHNEFSKASFGSGPA--VEMIPKYAGVSPKDRCKLIQCAKIGIGYFFVLQPKV 659

QY 639 VDGTPCSPDSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGDGGSGCSKQSGSPKFRFYG 698
 DB 660 VDGTPCSPDSTSVQVQGVQVAGCDRIIDSXKKFDKCGVCGGNGSTCKKISGVSPTSAPG 719

QY 699 YNNVVTIPAGATHILVROQGNPHRS--IYLALKLPDGSYALNGEYTLMPSPDVLVPCAV 756
 DB 720 YHDIITPTGATNIEVKQRNGSRNNGSFLAKAADGTIYILNGDYTLSTLEQDIMYKGV 779

QY 757 VSLRYSGATASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSPFVPRTPS--TPRPTPQ 815
 DB 780 V-LRYSGSSAALERIRSFPLKEPLTIQVLTVGNALRPKIKYTFVVKKSGSFNAIPTFS 838

QY 816 DWL 818
Db 839 AWV 841

RESULT 7
US-09-445-023A-1
; Sequence 1, Application US/09445023A
; Patent No. 6565858
; GENERAL INFORMATION:
; APPLICANT: Hirose, Kunitaka
; APPLICANT: Inoguchi, Eiji
; APPLICANT: Hakozaiki, Michinori
; APPLICANT: Ishioka, Keiko
; APPLICANT: Ishida, Yukako
; APPLICANT: Matsushima, Kouji
; APPLICANT: Kuno, Kouji
; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
; FILE REFERENCE: Q57092
; CURRENT APPLICATION NUMBER: US/09/445, 023A
; PRIOR FILING DATE: 1999-12-03
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 727
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-445-023A-1

Query Match 43.7%; Score 1998.5; DB 4; Length 727;
Best Local Similarity 57.5%; Pred. No. 2.2e-142; Indels 7; Gaps 6;
Matches 353; Conservative 105; Mismatches 149;

QY 209 RAKRFASLSRFVETLVVADDDKMAAFHAGLKRLLTVMAAAKAFKHPHSIRNPVSLVVR 268
Db 9 RKRFVSSPRVETMLVADQSMAEFHGSLKHYLLTLFVAARLYKHPHSIRNSVSLVVVK 68

QY 269 LVILGSGEGPQVPSAAOTLRSFCWQGLNTPEDSDPDHPTALLFTRODLGVSTCD 328
Db 69 ILVHDEQKPEVTSNAALTNRNFCWQKHNPPSDRDAEYDTHLFTRODLGVSTCD 128

QY 329 TLGMADVGTCDPARSCAIVEDDGLQSAFTAAHGLHGVFNMLHDSKPCISLNGPLSTR 388
Db 129 TLGMADVGTCDPSRSCSVIEDDGLQAAFTTAHGLHGVFNMPHDDAKQASLNG-VNQDS 187

QY 389 HVMAVPMHVDPEEPSPCSARFITDPLDNGYGHCLLDKPEAPLHPVTFFPGKYDADRQ 448
Db 188 HWASMLNLSHSPWSPCSAYMITSFLDNGHGECLMDKPEQNPQLPGDLPGTLYDANQ 247

QY 449 CQLTFGDSRHCPQLPPPCAALWCSGHLNGHAWCQTKHSPWADGTPCGPAQCMGRCULH 508
Db 248 CQTFGEDSKHCPDAAASTCTLWCTSGVLVVCQTKHFPWADGTSCEGKWCINGKCVN 307

QY 509 MDQLQDFNTPQAGGWPWPGWDCSRTCGGVQFSSRDCTRPVPRNGKYCEGRTRFRS 568
Db 308 KTRDKHFDTPFHGSGWPGWDCSRTCGGVQVYTWRECDNVPVKNKGKYCEGRVYRS 367

QY 569 CNTEDCPTGSALTFRFEEQCAAVNHRDLDL-FKSPFGPMVPRYTGVAPODQCKLTCQARA 627
Db 368 CNLEDCPDNNGKTFREEQCAHNEFSAFSGSPA-VENIPKYAGVSPKDRCKLICQAKG 426

QY 628 LGYVYVLEPRVVDGTPCSPDSSSVQVQRCIHAGCDRIIGSKKPKDKMVCVCGDGGCSK 687
Db 427 IGVYVFLQPKVVDGTPCSPDSTSVQVQCVKAGCDRIIDSKKPKDKVCGVCGNGSTCKK 486

QY 688 QSGSFRKFRYGYNNVVTIPAGATHILVROQGNPHRS--LYLAKLPDGSYALNGEYTL 745
Db 487 ISGSVTSKAPGVHDIVITPTGATNIEVKQRNGSRNNGSFLAIKAADGTLYLNGDYTL 546

QY 746 PSPTDVVLFVAVSLRYSGATAASETLSHGHPLAQPLTLQVLVAGNQDTRLRYSFVPRP 805
Db 547 TLEQDIMYKGVV-LRYSGSSAALERIRSPSPLEKPLTIQVLTGVNLRPKIKYTFVKKK 605

QY 806 TFS-TPRTPFDWL 818
Db 606 KESFNAIPTFSAWV 619

RESULT 8
US-09-445-023A-12
; Sequence 12, Application US/09445023A
; Patent No. 6565858
; GENERAL INFORMATION:
; APPLICANT: Hirose, Kunitaka
; APPLICANT: Inoguchi, Eiji
; APPLICANT: Hakozaiki, Michinori
; APPLICANT: Ishioka, Keiko
; APPLICANT: Ishida, Yukako
; APPLICANT: Matsushima, Kouji
; APPLICANT: Kuno, Kouji
; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical
; FILE REFERENCE: Q57092
; CURRENT APPLICATION NUMBER: US/09/445, 023A
; PRIOR FILING DATE: 1999-12-03
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 727
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-445-023A-12

Query Match 43.5%; Score 1986; DB 4; Length 727;
Best Local Similarity 56.1%; Pred. No. 2e-141; Indels 6; Gaps 5;
Matches 348; Conservative 111; Mismatches 155;

QY 203 PS-PRPRRAKRASLSRFVETLVVADDDKMAAFHAGLKRLLTVMAAAKAFKHPHSIRNP 261
Db 2 PSQSGSIRKRVSSPRVETMLVADQSMADFHGSLKHYLLTLFVAARLYKHPHSIRNS 61

QY 262 VSLVTRLVILGSGEGPQVPSAAOTLRSFCWQGLNTPEDSDPDHPTALLFTRODL 321
Db 62 ISLVVKKILVYEEQKPEVTSNAALTNRNFCWQKHNPPSDRDAEYDTHLFTRODL 121

QY 322 CGVSTCDTLGMADVGTCDPARSCAIVEDDGLQSAFTAAHGLHGVFNMLHDSKPCISLN 381
Db 122 CGSHTCDTLGMADVGTCDPSRSCSVIEDDGLQAAFTTAHGLHGVFNMPHDDAKHCA 181

QY 382 GPLSTSRHVPMAVPMHVDPEEPSPCSARFITDPLDNGYGHCLLDKPEAPLHPVTFFPGK 441
Db 182 G-VSGDLSHMLMSLSLSDHSPWSPCSAYMITSFLDNGHGECLMDKPEQNPQLPGD 240

QY 442 DYDADRQCOLTGPDSRHCPQLPPPCAALWCSGHLNGHAWCQTKHSPWADGTPCGPAOAC 501
Db 241 LYDADRQCOLTGPDSRHCPQLPPPCAALWCSGHLNGHAWCQTKHSPWADGTPCGPAOAC 300

QY 502 MGRCLHMDQLQDFNTPQAGGWPWPGWDCSRTCGGVQFSSRDCTRPVPRNGKYCEG 561
Db 301 VSGKCVNKTDMKHFAFPVHSGWPGWDCSRTCGGVQVYTWRECDNVPVKNKGKYCEG 360

QY 562 RTRFRSCNTEDCPTGSALTFRFEEQCAAVNHRDLDL-FKSPFGPMVPRYTGVAPODQCKL 621
Db 361 KEVRYRSCNTEDCPTGSALTFRFEEQCAHNEFSAFSGSPA-VENIPKYAGVSPKDRCKL 420

QY 622 TCQARALGYVYVLEPRVVDGTPCSPDSSSVQVQRCIHAGCDRIIGSKKPKDKMVCVCGD 681
Db 421 TCQARALGYVYVLEPRVVDGTPCSPDSTSVQVQCVKAGCDRIIDSKKPKDKMVCVCGD 480

QY 682 GSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVROQGNPHRS--LYLAKLPDGSYALN 739

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Db 481 GSTCKQMSGIVSTRPGYHDIWIPAGATNIEVKHNRQSGSRNNGSFLAIRADGTIILN 540
QY 740 GRYTLMPSTDDVVLPGAVSLRYSGATAASETLSGHGFLAQPITLQVLVAGNQDTRLRYS 799
Db 541 GNFTLSTLQDLTKGTV-LRYSGSAALEIRSFSPLEKPLTIQVLMVGHALRPKIKPT 599
QY 800 FVPRPTPS-TPRPTPDWL 818
Db 600 YFMKKKTESFNAIPTFSEW 619

RESULT 9
US-10-009-332-1
; Sequence 1, Application US/10009332
; Patent No. 6716613
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; APPLICANT: Kazusa DNA Research Institute
; TITLE OF INVENTION: NOVEL METALLOPROTEASE HAVING AGGREGANASE ACTIVITY
; FILE REFERENCE: Q67541
; CURRENT APPLICATION NUMBER: US/10/009,332
; CURRENT FILING DATE: 2001-12-10
; PRIOR FILING DATE: 1999-11-11
; PRIOR APPLICATION NUMBER: JPA 11-321740
; PRIOR APPLICATION NUMBER: JPA 2000-144020
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 950
; TYPE: PRI
; ORGANISM: Homo sapiens
US-10-009-332-1

Query Match 41.9%; Score 1917; DB 4; Length 950;
Best Local Similarity 46.3%; Pred. No. 4.5e-136;
Matches 381; Conservative 123; Mismatches 267; Indels 52; Gaps 16;

QY 37 LLLLLLASLLPSARLASPLPREBEIVPEKLSGVL-----PGSGAPARLLCRLQAF 88
Db 1 MLLLGILTLAFAGTAGGFPEREVVVPIRLDPDINGRRYYWRGPDSDGQGLIFQITAF 60

QY 89 GETLLELEODSGVQVEGLTVQVIGQAPE-LLGGAEP--GTLYLTGTINGDPESVASLHWD 145
Db 61 QEDFYHLTDAQFLAPAFSTEHLGVLPQLGTGSSDLRRCFYSGDVNAEPDFAAVSLC 120

QY 146 GGALLGVLYRGAEHLHQLPLEGGTPNSA--GGPGAHLRRK-----SPASGGGPMCNV--- 196
Db 121 GG-LRGAFYRGAEYVISPLPNASAPAAQRNSQGAHLQRRGVPGSGDPTSRGCVASG 179

QY 197 -----KAPLGSPPRRP--RAKRPASLSRFVETLVVADDKMAAFHAGLX 239
Db 180 WNPAILRALOPYKPRRAGFSGESRRRSRAKRFVSIPIRYVETLVVADDESVMVPHGADLE 239

QY 240 RYLLTVMAAARAKFKHPSIRNPVSLVTRVLVILSGEGPOVGPSPAATLRSFCAMQGL 299
Db 240 HYLLTLATARLYRHPSILNPINIVVVKVLLLRDSSGPKVTGNAALTLENFCAMQKQL 299

QY 300 NTPEDSDPDHPTDAILFTRQDLGVSTCDTLGMAADVGTCDPARSCAIVEDDGLQSAFTA 359
Db 300 NKVSDKHPEYWDTAILFTRQDLGCATCDTLGMAADVGTMCDPKESCSVIEDDGLPSAFT 359

QY 360 AHELGHVFMHLDNSKPCISLNGPLSTRVMAVPMVAHVDPPEEWPSCSAFIITFDLDNG 419
Db 360 AHELGHVFMHLDNSKPCISLNGPLSTRVMAVPMVAHVDPPEEWPSCSAFIITFDLDNG 418

QY 420 YGHCILLDKPEAPLHLVPTFPCKDYADRCQCOLTFGPDSSRHCPQLPPPCAALWCSCHLNGH 479
Db 419 HGDCLLOQPSKPISLPEDLPASVTLSSQCELAFGVGSKPCPYM-QYCTKLWCTGKAKGQ 477

QY 480 AMCQTKHSPWADGTPCGPAQCMGRCCLHMDQLQDFNIPQAGGWPWGPWGDGCSRTCGG 539
Db 480 AMCQTKHSPWADGTPCGPAQCMGRCCLHMDQLQDFNIPQAGGWPWGPWGDGCSRTCGG 539

Db 478 MVCQTRHPFWADGTSCEGKCLKGACVERNLNKHRVD--GSWAKWDPYGPCSRTCGG 535
QY 540 VOFSSRDCTRPVPRNGKYGCEGRRTRFRSCNTEDCP-TGSALTFFREEQCAA---YNHRTD 595
Db 536 VOLARQCTNTPANGKYGCEGVRVYKYSNLEPCPSSASGKSFREEQCEAFNGYNHSTN 595
QY 596 LFKSPFGPMDWVPRYTVGAPQDCKLTCAORALGYYVLEPRVVDGTCPSPSSSVCVQG 655
Db 596 RLTL---AVAWPKYSVSPRDKCKLICRANGTYFYVLAPKVVVDGTLTCLSPDSTSVCVQG 652
QY 656 RCIHAGCDRIIGSKKKFKDKCMVCGDGGSCSKQSGSKERKRYGYNVVTIPAGATHILVR 715
Db 653 KCIKAGCDNLGSKKRFDKGCVCGDNKCKKVTGLFTKPMHGYNFVVAIPAGASIDIR 712
QY 716 QQGNPG--HRSYILALKLPGSYALNGEYTLMPSPDVTVVLPAGAVSLRYSGATAASETLSG 773
Db 713 QRGYKGLIGDDNYLALKNSQGYKLLNGHFVVSVERDLVVKGSL-LRYSGTGTAVESLQA 771
QY 774 HGPLAQPLTQVLVAGNQDTRLRYSFFVPRPTPTPTPOD 816
Db 772 SRPILPLETVLELVSGKMTPPRVRYSFYLPKEPREDKSHPKD 814

RESULT 10
US-09-369-364A-9
; Sequence 9, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 9
; LENGTH: 905
; TYPE: PRI
; ORGANISM: Mus musculus ADAMTS-8
US-09-369-364A-9

Query Match 39.9%; Score 1824; DB 3; Length 905;
Best Local Similarity 44.2%; Pred. No. 4.5e-129;
Matches 373; Conservative 134; Mismatches 233; Indels 104; Gaps 26;

QY 36 WLLLLLASLLPSARLASPLP-----REEEIVPEKLSGVLPGSGAPARLLCRLQAF 88
Db 10 WPFLLLLLQLPPLPVCGAPAGPGTGAQASELVVTRLPESA-----SELAFHLSAF 62

QY 89 GETLLELEODSGVQVEGLTVQVIGQAPELLGGAEP---GTLYLTGTINGDPESVASLH-- 143
Db 63 GQGFVRLAPDASFLAPEFKIERLGGSSAAAGG-EPGLRGCFSGTVNGERESLAAMSCV 121

QY 144 --WDGALLGVLYRGAEHLHQLPLEG--TNN--SAGPGAHLRRKSP----- 186
Db 122 AGWSGSFLA-----GEEFTIQQAGDSLQDHLQWRWPGQ---RREDPGLAAAEVFP 173

QY 187 -----ASQG-----PMCNKAPLGSPPRRRAKRF 213
Db 174 LPQGLEWEVMGNGQGOERSDNEDKKQDEKGLLKETEDSRKVPFPFGSKT-----RSKRF 229

QY 214 ASLSRFVETLVVADDKMAAFHAGLKYLLTVMAAARAKFKHPSIRNPVSLVTRVLVILG 273
Db 230 VSEARFVETLVVADAMAAFYGTDLQNHILTVMSMAARIYKHPISIRSNVLVVKVLIVE 289

QY 274 SGEGPOVGPSPAATLRSFCAMQORGLNTPEDSDPDHPTDAILFTRQDLGV-STCDTLGM 332
Db 290 KERWGPVSDNGGLTLENFCNSWQRFNKPSDRHPEHYDTAILFTRQFGKGEQCDTLGM 349

QY 333 ADVGTVCDDPARSCAIVEDDGLQSAFTAHELGHVFMHLDNSKPCISLNGPLSTRVMA 392
Db 333 ADVGTVCDDPARSCAIVEDDGLQSAFTAHELGHVFMHLDNSKPCISLNGPLSTRVMA 392
```

350 ADVGTICDPKSCSVIKDGLQAAYTLAHELGHVLSMPHDDKPCVRLFGPMG-KYHMA 408
 393 PYMAHVDPPEPSPCSAREITFDLNGYGHCLLDKPEALPLHLPVTPPGKD--YDADROCO 450
 409 PFFIHWKTLWSPCSAVLTLLDGHGCLLDAPTSVLPFTGLPGHSTIYELDQCK 468
 451 LTFGDSRHCP--QLPPPCAALWCSGHLNG-HAMCOTKHP--WADGTPCGPAQACMGOR 505
 469 QIFGDFRHCNPTSVEBICVQL-CARHRSDDEPICHTKNGSLILWADGTPCGFGLCLDGS 527
 506 CLHMDLOLQFNIPQAGGWPMPGDCSRTCCGGVQFSSRDCTRPVPRNGKCYCEGRRTR 565
 528 CVLKEDVENPKAVVDGDFWPMGQCSRTCCGGIQFSNRECDNPMQNGRPFCLGERVK 587
 566 FRSCNTEDCPTGSALTFRREEQCA--AYNHRITDLFKSPGPMDDWVPRTYGVAPQDOCKLT 622
 588 YQSCNTEECPP-NGKSFREQCEKYNVNH-TDLGNF--LQWPKYSGVSPDRCKLF 642
 623 COARALGYVYVLEPRVVDGTPCSPDSSSVQVQGRCHHAGCDRIIGSKKFKDKMVCVGGDG 682
 643 CRARGRSEBKFVPEAKVIDGTGLGPDFTLSICVRGQCVKAGCDHVNWSPKLDKCGVCGGKG 702
 683 SCSCSOGSFRFRGYNNVVTIPAGATHILVROQGNPHGRS--IYLALKLPDGSYALNG 740
 703 TACRKISGFTFPGSYNDIVTIPAGATNIDVKORSHPGVRNDGSYALKTANGQYLLNG 762
 741 EYTLMPSPDVLVPGAVSLRYSGATAASETLSGHGPLAOPLTLOVL-VAGNPQDTRLRYS 799
 763 NLAINAIEQDILVKGTI-LKYSGSMTALRLQSFQALPEPLTVQLLTVSGEVFPKRYT 821
 800 FVFP 803
 822 FVFP 825

RESULT 11
 US-09-130-491-13
 ; Sequence 13, Application US/09130491
 ; Patent No. 6416974
 ; GENERAL INFORMATION:
 ; APPLICANT: Holtzman, Douglas A.
 ; APPLICANT: Goodearl, Andrew D.J.
 ; TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
 ; FILE REFERENCE: 09404/041001
 ; CURRENT APPLICATION NUMBER: US/09/130,491
 ; CURRENT FILING DATE: 1998-08-07
 ; EARLIER APPLICATION NUMBER: US 60/058,108
 ; EARLIER FILING DATE: 1997-09-05
 ; EARLIER FILING DATE: 1997-08-06
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 13
 ; LENGTH: 608
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-130-491-13

Query Match 39.2%; Score 1793.5; DB 4; Length 608;
 Best Local Similarity 56.5%; Pred. No. 5.3e-127;
 Matches 313; Conservative 97; Mismatches 137; Indels 7; Gaps 6;

QY 269 LVISGEGEGPOVGPAAOTLRSFCAWQRLNTPEDSDPHDPTALTFRQDLGCVSTCD 328
 DB 4 ILVIHDEQKGPVTSNAALTILNFCWQKHNPSPDRDAEHVDTALTFRQDLGCVSTCD 63
 QY 329 TLGMADVGTCDPARSCAIVEDGLQSAFTAHELGHVFNMLHNSKPCISLNGPLSTR 388
 DB 64 TLGMADVGTCDPSCSVIEDGLQAAFTTAHELGHVFNMPHDDAKQACASLNG-VNQDS 122
 QY 389 HWMAPVMAHVDEEPWSPCSARFITDNLNGYGHCLLDKPEALPLHLPVTPPGKDADQ 448
 DB 123 HWMASLNLDSQWSPSCSAYMITSFLDNGHGECLMDKQPNPIQLPGDLPGTSYDANRQ 182

QY 449 COLTFGDSRHCPQLPPPCAALWCSGHLNGHAMCOTKHPWADGTPCGPAQACMGORCLH 508
 DB 183 COFTFGEDSKHCPDAASTCTLWCTGSGVLVCQTKHFPWADGTSCEGKWCINGKCVN 242
 QY 509 MDLOLQFNIPQAGGWPMPGDCSRTCCGGVQFSSRDCTRPVPRNGKCYCEGRRTRFRS 568
 DB 243 KTDKRFHDFPFGSGWMPGDCSRTCCGGVQYTMRECDNPMVPRNGKCYCEGRRVYRS 302
 QY 569 CNTEDCPTGSALTFRREEQCAAYNHRITDL-FKSPGPMDDWVPRTYGVAPDOCKLTQCARA 627
 DB 303 CNLEDCPDNNGKTFREEQCEAHNEFSKASFGSGPA-VEWIPKYAGVSPDKRCKLIQAKG 361
 QY 628 LGYVYVLEPRVVDGTPCSPDSSSVQVQGRCHHAGCDRIIGSKKFKDKMVCVGGDGSCSK 687
 DB 362 IGYVFPVQPKVVDGTPCSPDSTSVQVQGVKAGCDRIIDSKKFKDKCGVCGGNGSTCKK 421
 QY 688 QSGSRFRFRGYNNVVTIPAGATHILVROQGNPHGRS--IYLALKLPDGSYALNGEYTL 745
 DB 422 ISGSVTSAPKGYHDIITIPIGATNIEVKORNGSRNNGSFLAIKAADGTIYLNGDYTLL 481
 QY 746 PSPTDVLVPGAVSLRYSGATAASETLSGHGPLAOPLTLOVL-VAGNPQDTRLRYSFVPRP 805
 DB 482 TLEQDIMYKGV-LRYSGSSAALERIRSFSLKEPLTIQVLTGVNLRPKIKITYPVKKK 540
 QY 806 TPS-TPRPTPDWL 818
 DB 541 KESFNAIPTFSAW 554

RESULT 12
 US-09-369-364A-2
 ; Sequence 2, Application US/09369364A
 ; Patent No. 6391610
 ; GENERAL INFORMATION:
 ; APPLICANT: Apte, Suneel
 ; APPLICANT: Hurskainen, Tiina L.
 ; APPLICANT: Hirohata, Satoshi
 ; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
 ; FILE REFERENCE: 26473/4007/10-30-00
 ; CURRENT APPLICATION NUMBER: US/09/369,364A
 ; CURRENT FILING DATE: 1999-08-06
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 930
 ; TYPE: PRT
 ; ORGANISM: mus musculus ADAMTS-5
 US-09-369-364A-2

Query Match 34.5%; Score 1576; DB 3; Length 930;
 Best Local Similarity 39.1%; Pred. No. 2.5e-110;
 Matches 348; Conservative 127; Mismatches 301; Indels 114; Gaps 22;

QY 31 LSW--LWMLLLLLASLL-----PSARLASPLP-----RREIV 62
 DB 3 LEWASILLLLLSASCLSLAADSAPAAPODKTRQPAQAAAAAEPDQPGETERGHL 62
 QY 63 FP---EKLNGSVL-----PGSGAPARLLCRLOAFGETLLELEODSGVQVGLTVQYL 112
 DB 63 QPLAGQRSGGVHNDIQLYSGGKGVYL---VYAGRRRLDLDERDDTVGAAG-SIVTA 118
 QY 113 GQAPELLGABEGTYLTGTINGDPESVASLHWGSGALLGVQVRGAELHLQPLEGG--- 168
 DB 119 GGLSASSGHRCHCFRGTVDSPLAVDFLCGG-LDGFVAVKHARYTLKPLLRGSWAE 177
 QY 169 -----TPNSAGG-----PGAH1-LRKSPASGQ 190
 DB 178 YERIYDGSRLHVNREBFGFEALPPRASCETPASPSGQESPSPVHSRRRSALAPQ 237
 QY 191 GPMCNVAPLGSFSPRP--RRAKRRFASLSRFVETLVVADDKMAAFHAGLKYLLTMAA 248
 DB 238 LLDHSAFSPSGNAGPQTWRRRRRSISRARQVELLVDSSMARMYGRGLHYLLTMAI 297

Best Local Similarity 41.2%; Pred. No. 5.6e-109;
Matches 325; Conservative 120; Mismatches 258; Indels 85; Gaps 19;

QY 87 ARGETLLELEODSGVQVEGLTVQVILGQAPPELLGGAEP-----GTVLTGTINGDPESVAS 141
Db 93 AGRRFLDLDERLDSGVGTIAGF-----VPAGGTSAPWRHRSCHCFYRGTVGDASPRSLAV 145
QY 142 LHWGCGALGVLYQVGAELHLOPLEGG----- 168
Db 146 FDLGG-LDGFPAVKHARYTLKPLLRGPWAEBEKGRVYGGGSARILHVVYTBREGFSPEALP 204
QY 169 -----TPNSAGPGAHILRRKSPA-----SGQGPC-----NVKAPLSPSPRP--RRA 210
Db 205 PRASCETP--ASTPEAH---EHAPAHNSPNSGRAALASQLLDQSALSAGSGSPQTWRRR 259
QY 211 KFPASLSRFEVETLVVADDKMAAFHAGLAKRYLLTWMAAAKAFKPSIRNPVSLVTVRLV 270
Db 260 RRSISRARQVELLLVADASMARLYGRLOHLYLLTLASIANRLYSHASINHLRLAVKVV 319
QY 271 ILGSGEGPQVGPSSAAQTLRSFCAWORGLNTPEDSDPHFDFTAILFTRODLGCVSTCDTL 330
Db 320 VLGDGDKSLEVSNAATLLKNFKWQHONQDDEEHYDAALLFTREDLCGHSCDYL 379
QY 331 GMADVTCDPARSCAIVDDGLQSAFTAAHBLGHVFNMLHNSKPCISLNGPLSTSRHV 390
Db 380 GMADVGTICSPERSCAVIEDDGLHAAFTVAHEIGHLLGLSHDSDSKFCEETFGSTEDKR-L 438
QY 391 MAPVMAHVDPPEPWPSCSARFTDFLDNGYGHCLLDKPEAPLHLPVTFPGKYDADROCC 450
Db 439 MSILTSIDASKPWSKCTSATITEFLDDGHGNCLLDLPKQILGPBELPGQTYDATQCCN 498
QY 451 LTFGPDSPHCPOLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCGPAQACMGRCCLHMD 510
Db 499 LTFGEYSVCPGM-DVCARLWCAVVRQGMVCLTKKLPAVEGTPCKGKRICLOGKCVDTK 557
QY 511 QIQDNFIPOAGWGPMPGDCSRTCGGVQFSSRDCTRPVPRNGGKYCEGRTRFRSCN 570
Db 558 KKKYTSSTSHGNWGSWGSQCSRSQCGGVQPAYRHNNPAPRNNGRYCTGKRAIYRSCS 617
QY 571 TEDCTGSALTREBQCAAYN-HRTDL--FKSFPFGPMWVRYTGVAPODCKLTQCARA 627
Db 618 LMPCCPP-NGKSPRHEQCEAKNGYQSDAKGVKTF---VEWVPKYAGVLPADVCKLTCKRAG 673
QY 628 LGYVYVLEPRVVDGTPCSPDSSVQVQRCIAGCDRIIGSKKKFKCMVCGDGGSGCSK 687
Db 674 TGYVYVFSKVTGTECRYSNVSVRGKCVRTGCDIIGSKLOYDKCGVCGDSSCTK 733
QY 688 QSGSFRKFRYGNVNVVITIPAGATHILVRQ--QGNPGHRSIYLALKLPDGSYALNGEYTL 745
Db 734 IVGTENKSKGYTDVVRIPGATHIKVRFKAKDQTRFTAYLALKKKNGEYLINGKYMIS 793
QY 746 PSPTDVLPGVSLRSGATASETLSHGPLA--QPLTLQVLVAGNPODTRLRYSFVFP 803
Db 794 TSETIIDINGTV-MNYSWMSHRDDFLHGMGYSATKEILIVQILATDPTKPLDVRYSFFVFP 852
QY 804 RPTPSTPR 811
Db 853 K--KSTPK 858

Search completed: April 1, 2005, 12:33:57
Job time : 49 secs

QY 142 LHWGCGALGVLYQVGAELHLOPLEGG----- 168
Db 146 FDLGG-LDGFPAVKHARYTLKPLLRGPWAEBEKGRVYGGGSARILHVVYTBREGFSPEALP 204
QY 169 -----TPNSAGPGAHILRRKSPA-----SGQGPC-----NVKAPLSPSPRP--RRA 210
Db 205 PRASCETP--ASTPEAH---EHAPAHNSPNSGRAALASQLLDQSALSAGSGSPQTWRRR 259
QY 211 KFPASLSRFEVETLVVADDKMAAFHAGLAKRYLLTWMAAAKAFKPSIRNPVSLVTVRLV 270
Db 260 RRSISRARQVELLLVADASMARLYGRLOHLYLLTLASIANRLYSHASINHLRLAVKVV 319
QY 271 ILGSGEGPQVGPSSAAQTLRSFCAWORGLNTPEDSDPHFDFTAILFTRODLGCVSTCDTL 330
Db 320 VLGDGDKSLEVSNAATLLKNFKWQHONQDDEEHYDAALLFTREDLCGHSCDYL 379
QY 331 GMADVTCDPARSCAIVDDGLQSAFTAAHBLGHVFNMLHNSKPCISLNGPLSTSRHV 390
Db 380 GMADVGTICSPERSCAVIEDDGLHAAFTVAHEIGHLLGLSHDSDSKFCEETFGSTEDKR-L 438
QY 391 MAPVMAHVDPPEPWPSCSARFTDFLDNGYGHCLLDKPEAPLHLPVTFPGKYDADROCC 450
Db 439 MSILTSIDASKPWSKCTSATITEFLDDGHGNCLLDLPKQILGPBELPGQTYDATQCCN 498
QY 451 LTFGPDSPHCPOLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCGPAQACMGRCCLHMD 510
Db 499 LTFGEYSVCPGM-DVCARLWCAVVRQGMVCLTKKLPAVEGTPCKGKRICLOGKCVDTK 557
QY 511 QIQDNFIPOAGWGPMPGDCSRTCGGVQFSSRDCTRPVPRNGGKYCEGRTRFRSCN 570
Db 558 KKKYTSSTSHGNWGSWGSQCSRSQCGGVQPAYRHNNPAPRNNGRYCTGKRAIYRSCS 617
QY 571 TEDCTGSALTREBQCAAYN-HRTDL--FKSFPFGPMWVRYTGVAPODCKLTQCARA 627
Db 618 LMPCCPP-NGKSPRHEQCEAKNGYQSDAKGVKTF---VEWVPKYAGVLPADVCKLTCKRAG 673
QY 628 LGYVYVLEPRVVDGTPCSPDSSVQVQRCIAGCDRIIGSKKKFKCMVCGDGGSGCSK 687
Db 674 TGYVYVFSKVTGTECRYSNVSVRGKCVRTGCDIIGSKLOYDKCGVCGDSSCTK 733
QY 688 QSGSFRKFRYGNVNVVITIPAGATHILVRQ--QGNPGHRSIYLALKLPDGSYALNGEYTL 745
Db 734 IVGTENKSKGYTDVVRIPGATHIKVRFKAKDQTRFTAYLALKKKNGEYLINGKYMIS 793
QY 746 PSPTDVLPGVSLRSGATASETLSHGPLA--QPLTLQVLVAGNPODTRLRYSFVFP 803
Db 794 TSETIIDINGTV-MNYSWMSHRDDFLHGMGYSATKEILIVQILATDPTKPLDVRYSFFVFP 852
QY 804 RPTPSTPR 811
Db 853 K--KSTPK 858

RESULT 15
US-10-247-685-15
; Sequence 15, Application US/10247685
; Patent No. 6753176
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGREGAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909D
; CURRENT APPLICATION NUMBER: US/10/247,685
; CURRENT FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-247-685-15

Query Match 34.1%; Score 1558; DB 4; Length 930;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 12:30:41 ; Search time 149 Seconds
(without alignments)
1862.706 Million cell updates/sec

Title: US-09-634-287E-2

Perfect score: 4570

Sequence: 1 MSQTSHPGRGLAGRWLWGA.....LHRRQAILELRRPWAGRK 837

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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19: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	4570	100.0	837	14	US-10-247-685-2
2	4570	100.0	837	16	US-10-408-765A-1348
3	4570	100.0	837	16	US-10-628-432-1
4	4567	99.9	846	16	US-10-628-432-29
5	4566	99.9	837	15	US-10-358-283-11
6	4563	99.8	837	10	US-09-946-374-317
7	4563	99.8	837	13	US-10-052-586-352
8	4563	99.8	837	14	US-10-174-590-352
9	4563	99.8	837	14	US-10-176-758-352
10	4563	99.8	837	14	US-10-175-737-352
11	4563	99.8	837	14	US-10-174-581-352
12	4563	99.8	837	14	US-10-176-483-352
13	4563	99.8	837	14	US-10-176-749-352
14	4563	99.8	837	14	US-10-176-749-352

14	4563	99.8	837	14	US-10-176-914-352	Sequence 352, App
15	4563	99.8	837	14	US-10-176-915-352	Sequence 352, App
16	4563	99.8	837	14	US-10-173-706-352	Sequence 352, App
17	4563	99.8	837	14	US-10-175-738-352	Sequence 352, App
18	4563	99.8	837	14	US-10-175-752-352	Sequence 352, App
19	4563	99.8	837	14	US-10-176-482-352	Sequence 352, App
20	4563	99.8	837	14	US-10-176-757-352	Sequence 352, App
21	4563	99.8	837	14	US-10-176-913-352	Sequence 352, App
22	4563	99.8	837	14	US-10-180-552-352	Sequence 352, App
23	4563	99.8	837	14	US-10-180-557-352	Sequence 352, App
24	4563	99.8	837	14	US-10-173-700-352	Sequence 352, App
25	4563	99.8	837	14	US-10-174-572-352	Sequence 352, App
26	4563	99.8	837	14	US-10-174-579-352	Sequence 352, App
27	4563	99.8	837	14	US-10-174-582-352	Sequence 352, App
28	4563	99.8	837	14	US-10-174-588-352	Sequence 352, App
29	4563	99.8	837	14	US-10-175-739-352	Sequence 352, App
30	4563	99.8	837	14	US-10-175-740-352	Sequence 352, App
31	4563	99.8	837	14	US-10-175-743-352	Sequence 352, App
32	4563	99.8	837	14	US-10-176-488-352	Sequence 352, App
33	4563	99.8	837	14	US-10-176-492-352	Sequence 352, App
34	4563	99.8	837	14	US-10-176-747-352	Sequence 352, App
35	4563	99.8	837	14	US-10-176-750-352	Sequence 352, App
36	4563	99.8	837	14	US-10-176-985-352	Sequence 352, App
37	4563	99.8	837	14	US-10-176-987-352	Sequence 352, App
38	4563	99.8	837	14	US-10-176-992-352	Sequence 352, App
39	4563	99.8	837	14	US-10-176-993-352	Sequence 352, App
40	4563	99.8	837	14	US-10-184-658-352	Sequence 352, App
41	4563	99.8	837	14	US-10-176-991-352	Sequence 352, App
42	4563	99.8	837	14	US-10-173-695-352	Sequence 352, App
43	4563	99.8	837	14	US-10-173-697-352	Sequence 352, App
44	4563	99.8	837	14	US-10-173-705-352	Sequence 352, App
45	4563	99.8	837	14	US-10-174-576-352	Sequence 352, App

ALIGNMENTS

RESULT 1

US-10-247-685-2
; Sequence 2, Application US/10247685
; Publication No. US20030108998A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGREGAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909D
; CURRENT APPLICATION NUMBER: US/10/247,685
; CURRENT FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-247-685-2

Query Match 100.0%; Score 4570; DB 14; Length 837;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 837; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSQTSHPGRGLAGRWLWGAQPCLLLPVPLSWLWLLLLLLASLLPSARLASPLPREE	60
DB	1	MSQTSHPGRGLAGRWLWGAQPCLLLPVPLSWLWLLLLLLASLLPSARLASPLPREE	60
QY	61	IYFPEKLINGSVLPGSGAPARLLCRQAQFCTLLLELLEQDSGVQVQVGLTVQYLGAQAPELLG	120
DB	61	IYFPEKLINGSVLPGSGAPARLLCRQAQFCTLLLELLEQDSGVQVQVGLTVQYLGAQAPELLG	120
QY	121	GAEPGYLTGTNGDPESVASLHWDCGALLGVLYRGAELHLQPLEGGTSPNSAGGFGAHI	180
DB	121	GAEPGYLTGTNGDPESVASLHWDCGALLGVLYRGAELHLQPLEGGTSPNSAGGFGAHI	180
QY	181	LRRKSPASQGGPMCNVKAFLGSPSPRRPRKAFASLSRFVETLVVADDKMAAFHAGLKKR	240

Db	181	LRRKSPASQGGPMCNVKAFLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKR	240
QY	241	YLLTVMMAAAKAFKHPISIRNPVSLVTRVLVILGSEEGPQVGPSSAAQTILRSCAWORGLN	300
Db	241	YLLTVMMAAAKAFKHPISIRNPVSLVTRVLVILGSEEGPQVGPSSAAQTILRSCAWORGLN	300
QY	301	TPEDSDPHDFTAILTRQDLQCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAA	360
Db	301	TPEDSDPHDFTAILTRQDLQCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAA	360
QY	361	HELGHVFNMLHDSKPCISLNGPLSTRHVMAVMAHVDPEPWPSCSARFITDFLDNGY	420
Db	361	HELGHVFNMLHDSKPCISLNGPLSTRHVMAVMAHVDPEPWPSCSARFITDFLDNGY	420
QY	421	GHCLLDKPEAPLHPVTFPGKDYADRCQLTFGPDNRHCPQLPPPCAALWCSGHLNGHA	480
Db	421	GHCLLDKPEAPLHPVTFPGKDYADRCQLTFGPDNRHCPQLPPPCAALWCSGHLNGHA	480
QY	481	MCQTKHSPWADGTPCGPAQACMGGRCLHMDQLQDFNIPOAGGWPMPGWDGCSRTCGGV	540
Db	481	MCQTKHSPWADGTPCGPAQACMGGRCLHMDQLQDFNIPOAGGWPMPGWDGCSRTCGGV	540
QY	541	QFSSRDCTRPVPRNGGKYCEGRTRFRSCNTEDCPTGSALTFRBEOCAAYNHRITDLFKSF	600
Db	541	QFSSRDCTRPVPRNGGKYCEGRTRFRSCNTEDCPTGSALTFRBEOCAAYNHRITDLFKSF	600
QY	601	PGMDMWPRYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSSVCVQGRCIHA	660
Db	601	PGMDMWPRYTGVAPODQCKLTQARALGYVYVLEPRVVDGTPCSPDSSSVCVQGRCIHA	660
QY	661	GCDRIIGSKKKFKDKMVCVCGDGGSGCSKQSGSFRKFRFYGNVNVVTIPAGATHILVROQGNP	720
Db	661	GCDRIIGSKKKFKDKMVCVCGDGGSGCSKQSGSFRKFRFYGNVNVVTIPAGATHILVROQGNP	720
QY	721	GHRISYIALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSHGGLAOP	780
Db	721	GHRISYIALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSHGGLAOP	780
QY	781	LTLQVLVAGNPQDTRLRYSFVPRPTSTPRTPDQWLHRRRAQILLEILRRRPWAGRK	837
Db	781	LTLQVLVAGNPQDTRLRYSFVPRPTSTPRTPDQWLHRRRAQILLEILRRRPWAGRK	837
RESULT 2			
US-10-408-765A-1348			
; Sequence 1348, Application US/10408765A			
; Publication No. US20040101874A1			
; GENERAL INFORMATION:			
; APPLICANT: Ghosh, Soumitra S.			
; APPLICANT: Fahy, Eoin D.			
; APPLICANT: Zhang, Bing			
; APPLICANT: Gibson, Bradford W.			
; APPLICANT: Taylor, Steven W.			
; APPLICANT: Glenn, Gary M.			
; APPLICANT: Wattock, Dale E.			
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION			
; FILE REFERENCE: 660088.465			
; CURRENT APPLICATION NUMBER: US/10/408.765A			
; CURRENT FILING DATE: 2003-04-04			
; NUMBER OF SEQ ID NOS: 3077			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 1348			
; LENGTH: 837			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-408-765A-1348			
Query Match 100.0%; Score 4570; DB 16; Length 837;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 837; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	MSQTGSHGPRGLAGRWLWGAQPCILLPIVPLSWLWMLLLLLASLLPSARLASPLPREEE	60

Query Match 100.0%; Score 4570; DB 16; Length 837;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 837; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOTGSHPGRLAGRWLWGAQPCLLPIVPLSLVWMLLLLLASLPSARLASPLPREEE 60
DB 1 MSOTGSHPGRLAGRWLWGAQPCLLPIVPLSLVWMLLLLLASLPSARLASPLPREEE 60

QY 61 IVEPEKLSVLPVPGSGAPARLLCRLOAFGETLLELEQDSGVQVEGLTVQYLQAPPELLG 120
DB 61 IVEPEKLSVLPVPGSGAPARLLCRLOAFGETLLELEQDSGVQVEGLTVQYLQAPPELLG 120

QY 121 GAEPGYLTGTINGDPESVSLHWDGGLLVQYRGAEHLHLOPLEGGTNSAGGCAHI 180
DB 121 GAEPGYLTGTINGDPESVSLHWDGGLLVQYRGAEHLHLOPLEGGTNSAGGCAHI 180

QY 181 LRKSPASGQGPCNVCAPLGSPPRRRAKRFPASLSRFVETLVVADDKMAAFHAGLKR 240
DB 181 LRKSPASGQGPCNVCAPLGSPPRRRAKRFPASLSRFVETLVVADDKMAAFHAGLKR 240

QY 241 YLLTVMAAAKAFKHSIRNPVSLVTRVLVILGSGEGPQVPSAAQTLSFCWQORGLN 300
DB 241 YLLTVMAAAKAFKHSIRNPVSLVTRVLVILGSGEGPQVPSAAQTLSFCWQORGLN 300

QY 301 TPEDSDPDHFDTAILFTRODLGVSTCDTLGMADVGTCDPARSCAIVEDDGLQSAFTAA 360
DB 301 TPEDSDPDHFDTAILFTRODLGVSTCDTLGMADVGTCDPARSCAIVEDDGLQSAFTAA 360

QY 361 HELGHVFNMLHNSKFCISLNGPLSTRHVMAFVMAHVDPEEPWSPCSARFIFDLDNGY 420
DB 361 HELGHVFNMLHNSKFCISLNGPLSTRHVMAFVMAHVDPEEPWSPCSARFIFDLDNGY 420

QY 421 GHCLLDKPEAPLHLPTVTFPGDYADROQCLTFGPDSSRHCPLPPCAALWCSGHLNGHA 480
DB 421 GHCLLDKPEAPLHLPTVTFPGDYADROQCLTFGPDSSRHCPLPPCAALWCSGHLNGHA 480

QY 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWGPMGDCSRTCCGGV 540
DB 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWGPMGDCSRTCCGGV 540

QY 541 QFSRDCTRPVPRNGKCYCEGRTRFRSCNTEDCPTGSALTFRFEOCAAYNHRTDLFKSF 600
DB 541 QFSRDCTRPVPRNGKCYCEGRTRFRSCNTEDCPTGSALTFRFEOCAAYNHRTDLFKSF 600

QY 601 PGMDWVPRYTVGAPDQCKLTQARALGYVYVLEPRVVDGTPCSPDSSVCVQGRCIHA 660
DB 601 PGMDWVPRYTVGAPDQCKLTQARALGYVYVLEPRVVDGTPCSPDSSVCVQGRCIHA 660

QY 661 GCDRIIGSKKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVROQGNP 720
DB 661 GCDRIIGSKKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVROQGNP 720

QY 721 GHSRIYALKLPDGSVALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSHGGLAQP 780
DB 721 GHSRIYALKLPDGSVALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSHGGLAQP 780

QY 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPDWLHRRQAQILRLRRPWAGRK 837
DB 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPDWLHRRQAQILRLRRPWAGRK 837

RESULT 4

US-10-628-432-29
; Sequence 29, Application US/10628432
; Publication No. US20040142863A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Modified ADAMTS4 molecules
; FILE REFERENCE: AM101378
; CURRENT APPLICATION NUMBER: US/10/628,432
; CURRENT FILING DATE: 2003-07-29
; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 846
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: ADAMTS4 with active-site mutation
; US-10-628-432-29

Query Match 99.9%; Score 4567; DB 16; Length 846;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 836; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOTGSHPGRLAGRWLWGAQPCLLPIVPLSLVWMLLLLLASLPSARLASPLPREEE 60
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QY 61 IVEPEKLSVLPVPGSGAPARLLCRLOAFGETLLELEQDSGVQVEGLTVQYLQAPPELLG 120
DB 61 IVEPEKLSVLPVPGSGAPARLLCRLOAFGETLLELEQDSGVQVEGLTVQYLQAPPELLG 120

QY 121 GAEPGYLTGTINGDPESVSLHWDGGLLVQYRGAEHLHLOPLEGGTNSAGGCAHI 180
DB 121 GAEPGYLTGTINGDPESVSLHWDGGLLVQYRGAEHLHLOPLEGGTNSAGGCAHI 180

QY 181 LRKSPASGQGPCNVCAPLGSPPRRRAKRFPASLSRFVETLVVADDKMAAFHAGLKR 240
DB 181 LRKSPASGQGPCNVCAPLGSPPRRRAKRFPASLSRFVETLVVADDKMAAFHAGLKR 240

QY 241 YLLTVMAAAKAFKHSIRNPVSLVTRVLVILGSGEGPQVPSAAQTLSFCWQORGLN 300
DB 241 YLLTVMAAAKAFKHSIRNPVSLVTRVLVILGSGEGPQVPSAAQTLSFCWQORGLN 300

QY 301 TPEDSDPDHFDTAILFTRODLGVSTCDTLGMADVGTCDPARSCAIVEDDGLQSAFTAA 360
DB 301 TPEDSDPDHFDTAILFTRODLGVSTCDTLGMADVGTCDPARSCAIVEDDGLQSAFTAA 360

QY 361 HELGHVFNMLHNSKFCISLNGPLSTRHVMAFVMAHVDPEEPWSPCSARFIFDLDNGY 420
DB 361 HELGHVFNMLHNSKFCISLNGPLSTRHVMAFVMAHVDPEEPWSPCSARFIFDLDNGY 420

QY 421 GHCLLDKPEAPLHLPTVTFPGDYADROQCLTFGPDSSRHCPLPPCAALWCSGHLNGHA 480
DB 421 GHCLLDKPEAPLHLPTVTFPGDYADROQCLTFGPDSSRHCPLPPCAALWCSGHLNGHA 480

QY 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWGPMGDCSRTCCGGV 540
DB 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWGPMGDCSRTCCGGV 540

QY 541 QFSRDCTRPVPRNGKCYCEGRTRFRSCNTEDCPTGSALTFRFEOCAAYNHRTDLFKSF 600
DB 541 QFSRDCTRPVPRNGKCYCEGRTRFRSCNTEDCPTGSALTFRFEOCAAYNHRTDLFKSF 600

QY 601 PGMDWVPRYTVGAPDQCKLTQARALGYVYVLEPRVVDGTPCSPDSSVCVQGRCIHA 660
DB 601 PGMDWVPRYTVGAPDQCKLTQARALGYVYVLEPRVVDGTPCSPDSSVCVQGRCIHA 660

QY 661 GCDRIIGSKKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVROQGNP 720
DB 661 GCDRIIGSKKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVROQGNP 720

QY 721 GHSRIYALKLPDGSVALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSHGGLAQP 780
DB 721 GHSRIYALKLPDGSVALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSHGGLAQP 780

QY 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPDWLHRRQAQILRLRRPWAGRK 837
DB 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPDWLHRRQAQILRLRRPWAGRK 837

RESULT 5

US-10-358-283-11
; Sequence 11, Application US/10358283

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; Publication No. US20040054149A1
; GENERAL INFORMATION:
; APPLICANT: WYETH
; TITLE OF INVENTION: TRUNCATED AGGRECANASE MOLECULES
; FILE REFERENCE: 08702-0112-00000
; CURRENT APPLICATION NUMBER: US/10/358,283
; CURRENT FILING DATE: 2003-02-17
; PRIOR APPLICATION NUMBER: 60/354,592
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 11
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-358-283-11

Query Match          99.9%; Score 4566; DB 15; Length 837;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MSQTGSHPGRLAGRLWGAQPCLLPIVPLSLWMLLLLLLASLLPSARLASPLPREE 60
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DB 61 IVPEKLINGSVLPGSGTPARLLCRLQAFGETLLELEQDSGVQVEGLTVQYLQOAPPELLG 120
QY 121 GAEFGTYLTCTINGDPESVASLHWDGALLGVLYRGAELHQLPLEGGTSPNSAGGFGAHI 180
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DB 181 LRKSPASGGQPCNWKAPLGSPPRRRAKRPASLSRFVETLVVADDKMAAHHGAGLKR 240
QY 241 YLITVMAAAKAFKHSIRNPVSLVTRVLILSGEGPGVGPSSAAQTLSFCAWORGSLN 300
DB 241 YLITVMAAAKAFKHSIRNPVSLVTRVLILSGEGPGVGPSSAAQTLSFCAWORGSLN 300
QY 301 TPEDSDPDHFDTAILFTROQLCGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAA 360
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QY 361 HELGHVFNMLHDNSKPCISLNGPLSTRHVPMAHVDPPEPSPCSARPIITDFLDNGY 420
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DB 481 MCQTKHSPWADGTPCGPAQACMGRCLHMDQLQDFNIPQAGGWPMPGWDGCSRTCGGV 540
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QY 721 GHSIYIALKLPGSYALNGEYTLMPSPDVLPGAVSLRYSGATASETLSHGHPLAQP 780
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; RESULT 6
; US-09-946-374-317
; Sequence 317, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Fan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
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Query Match 99.8%; Score 4563; DB 10; Length 837;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 IVFPKINGSVLPFGGAPARLLCRLOAFGETLLELEQDSGVQVEGLTVQYLQAPPELLG 120

Db 61 IVFPKINGSVLPFGGAPARLLCRLOAFGETLLELEQDSGVQVEGLTVQYLQAPPELLG 120

Fri Apr 1 15:02:40 2005

us-09-634-287e-2.rapb

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RESULT 7
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 ; Sequence 352, Application US/10052586
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 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C1
 ; CURRENT APPLICATION NUMBER: US/10/052,586
 ; CURRENT FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266
 ; PRIOR FILING DATE: 1997-09-18
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/ PRIOR APPLICATION NUMBER: 60/085700
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/086023
/ PRIOR FILING DATE: 1998-05-18
/ PRIOR APPLICATION NUMBER: 60/086392
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/086486
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087098
/ PRIOR FILING DATE: 1998-05-28
/ PRIOR APPLICATION NUMBER: 60/087208
/ PRIOR FILING DATE: 1998-05-28
/ PRIOR APPLICATION NUMBER: 60/087609
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/087759
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/087827
/ PRIOR FILING DATE: 1998-06-03
/ PRIOR APPLICATION NUMBER: 60/088025
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/088028
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/088029
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/088033
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/088167
/ PRIOR FILING DATE: 1998-06-05
/ PRIOR APPLICATION NUMBER: 60/088202
/ PRIOR FILING DATE: 1998-06-05
/ PRIOR APPLICATION NUMBER: 60/088212
/ PRIOR FILING DATE: 1998-06-05
/ PRIOR APPLICATION NUMBER: 60/088217
/ PRIOR FILING DATE: 1998-06-05
/ PRIOR APPLICATION NUMBER: 60/088326
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/088655
/ PRIOR FILING DATE: 1998-06-09
/ PRIOR APPLICATION NUMBER: 60/088722
/ PRIOR FILING DATE: 1998-06-10

/ PRIOR APPLICATION NUMBER: 60/088738
/ PRIOR FILING DATE: 1998-06-10
/ PRIOR APPLICATION NUMBER: 60/088740
/ PRIOR FILING DATE: 1998-06-10
/ PRIOR APPLICATION NUMBER: 60/088811
/ PRIOR FILING DATE: 1998-06-10
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/ PRIOR APPLICATION NUMBER: 60/088825
/ PRIOR FILING DATE: 1998-06-10
/ PRIOR APPLICATION NUMBER: 60/088826
/ PRIOR FILING DATE: 1998-06-10
/ PRIOR APPLICATION NUMBER: 60/088861
/ PRIOR FILING DATE: 1998-06-11
/ PRIOR APPLICATION NUMBER: 60/088863
/ PRIOR FILING DATE: 1998-06-11
/ PRIOR APPLICATION NUMBER: 60/088876
/ PRIOR FILING DATE: 1998-06-11
/ PRIOR APPLICATION NUMBER: 60/089090
/ PRIOR FILING DATE: 1998-06-12
/ PRIOR APPLICATION NUMBER: 60/089105
/ PRIOR FILING DATE: 1998-06-12
/ PRIOR APPLICATION NUMBER: 60/089512
/ PRIOR FILING DATE: 1998-06-16
/ PRIOR APPLICATION NUMBER: 60/089514
/ PRIOR FILING DATE: 1998-06-16
/ PRIOR APPLICATION NUMBER: 60/089538
/ PRIOR FILING DATE: 1998-06-17
/ PRIOR APPLICATION NUMBER: 60/089598
/ PRIOR FILING DATE: 1998-06-17
/ PRIOR APPLICATION NUMBER: 60/089653
/ PRIOR FILING DATE: 1998-06-17
/ PRIOR APPLICATION NUMBER: 60/089908

Query Match 99.8%; Score 4563; DB 13; Length 837;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSQTGSHPGRGLAGRWLWGAQPCLLPIVPLSWLWLLLLASLLPSARLASPLPREE 60
Db 1 MSQTGSHPGRGLAGRWLWGAQPCLLPIVPLSWLWLLLLASLLPSARLASPLPREE 60
Qy 61 IVFPEKINGSVLPGSGAPARLLCRQAFCETLLELEQDSGVQVEGLTVQYLQAPPELLG 120
Db 61 IVFPEKINGSVLPGSGAPARLLCRQAFCETLLELEQDSGVQVEGLTVQYLQAPPELLG 120
Qy 121 GAEPGYLTGTINGDPESVASLHWGALLGVQYRGAELHLQPLEGGTPNSAGGPAHI 180
Db 121 GAEPGYLTGTINGDPESVASLHWGALLGVQYRGAELHLQPLEGGTPNSAGGPAHI 180
Qy 181 LRRKSPASQGGPMCNVKAFLGSPSPRRPRAKRFASLSRFVETLVVADDKMAAFHAGLKR 240
Db 181 LRRKSPASQGGPMCNVKAFLGSPSPRRPRAKRFASLSRFVETLVVADDKMAAFHAGLKR 240
Qy 241 YLLTWMAAAAKAFKPSIRNPVSLVVTRILVILGSGEGBQVGPSPAAQTLSFCAWORGLN 300
Db 241 YLLTWMAAAAKAFKPSIRNPVSLVVTRILVILGSGEGBQVGPSPAAQTLSFCAWORGLN 300
Qy 301 TPEDSDPHDFDTAILFTRODLGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAA 360
Db 301 TPEDSDPHDFDTAILFTRODLGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAA 360
Qy 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAVMAHVDPBPWSPSCSARFITDFLNGY 420
Db 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAVMAHVDPBPWSPSCSARFITDFLNGY 420
Qy 421 GHCLLDKPEAPLHLVPTFFPKDYDADRQCQLTFGPDPSRHCPLQPPPCAALWCSGHLNGHA 480
Db 421 GHCLLDKPEAPLHLVPTFFPKDYDADRQCQLTFGPDPSRHCPLQPPPCAALWCSGHLNGHA 480
Qy 481 MCQTKHSPWADGTPCGPAQACMGGRCLHMDQLQDFNIPQAGGWGMPGWGDCSRTCCGGV 540
Db 481 MCQTKHSPWADGTPCGPAQACMGGRCLHMDQLQDFNIPQAGGWGMPGWGDCSRTCCGGV 540
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Db 1 MSQTSHPGRGLAGRWLWGAQPCLLPIVPLSWLWLLLLASLLPSARLASPLPREB 60
Qy 61 IVFPEKLGSLVPGSGAPARLLCRLOAFGETLLEQDSGVQVGLTVQYLGQAPPELLG 120
Db 61 IVFPEKLGSLVPGSGAPARLLCRLOAFGETLLEQDSGVQVGLTVQYLGQAPPELLG 120
Qy 121 GAEPGTTLTGTINGDPESVASLHWDGALLGVLYQVGAELHLQPLEGGTPNSAGGPGAH 180
Db 121 GAEPGTTLTGTINGDPESVASLHWDGALLGVLYQVGAELHLQPLEGGTPNSAGGPGAH 180
Qy 181 LRRKSPASQGMPCNVKAPLGSPPRRPRRAKRFASLSRFVETLVVADDKMAAFHAGLKR 240
Db 181 LRRKSPASQGMPCNVKAPLGSPPRRPRRAKRFASLSRFVETLVVADDKMAAFHAGLKR 240
Qy 241 YLLTWMAAAKAFKPSIRNPVSLVTRVLVILGSGEGPQVGSAAQTLSFCAMQRLN 300
Db 241 YLLTWMAAAKAFKPSIRNPVSLVTRVLVILGSGEGPQVGSAAQTLSFCAMQRLN 300
Qy 301 TPEDSDPHDFDTAILFTRODLGCVSTCDTLGMADVTVCDPARSCAIVEDDGLQSAFTAA 360
Db 301 TPEDSDPHDFDTAILFTRODLGCVSTCDTLGMADVTVCDPARSCAIVEDDGLQSAFTAA 360
Qy 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAVMAHVDPEEPWPCSFARFTTDFLDNGY 420
Db 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAVMAHVDPEEPWPCSFARFTTDFLDNGY 420
Qy 421 GHCLLDKPEAPLHLVPTFGKDYDADROCOLTFGPDSSRHCPLPPCAALWCSGHLNGHA 480
Db 421 GHCLLDKPEAPLHLVPTFGKDYDADROCOLTFGPDSSRHCPLPPCAALWCSGHLNGHA 480
Qy 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWPWGMDCSRTCCGGV 540
Db 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWPWGMDCSRTCCGGV 540
Qy 541 QFSRDCTRPVPRNGKYCEGRTRFRSCNTEDCPTGSALTFRBQCAAYNHRITDLFKSF 600
Db 541 QFSRDCTRPVPRNGKYCEGRTRFRSCNTEDCPTGSALTFRBQCAAYNHRITDLFKSF 600
Qy 601 PGPMWVPRYTGVAPODQCKLTCQARALGYVYVLEPRVVDGTPCSPDSSSVCQGRCHIA 660
Db 601 PGPMWVPRYTGVAPODQCKLTCQARALGYVYVLEPRVVDGTPCSPDSSSVCQGRCHIA 660
Qy 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQGNP 720
Db 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQGNP 720
Qy 721 GHSIYLAALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSGHGPLAQP 780
Db 721 GHSIYLAALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSGHGPLAQP 780
Qy 781 LTLQVLVAGNPQDTRLRYSPFVPRPTPTPQDMLHRRQAIILEILRRRPWAGRK 837
Db 781 LTLQVLVAGNPQDTRLRYSPFVPRPTPTPQDMLHRRQAIILEILRRRPWAGRK 837
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RESULT 10

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US-10-175-737-352
; Sequence 352, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RIC50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 352
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-352
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Query Match 99.8%; Score 4563; DB 14; Length 837;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 MSQTSHPGRGLAGRWLWGAQPCLLPIVPLSWLWLLLLASLLPSARLASPLPREB 60
Db 1 MSQTSHPGRGLAGRWLWGAQPCLLPIVPLSWLWLLLLASLLPSARLASPLPREB 60
Qy 61 IVFPEKLGSLVPGSGAPARLLCRLOAFGETLLEQDSGVQVGLTVQYLGQAPPELLG 120
Db 61 IVFPEKLGSLVPGSGAPARLLCRLOAFGETLLEQDSGVQVGLTVQYLGQAPPELLG 120
Qy 121 GAEPGTTLTGTINGDPESVASLHWDGALLGVLYQVGAELHLQPLEGGTPNSAGGPGAH 180
Db 121 GAEPGTTLTGTINGDPESVASLHWDGALLGVLYQVGAELHLQPLEGGTPNSAGGPGAH 180
Qy 181 LRRKSPASQGMPCNVKAPLGSPPRRPRRAKRFASLSRFVETLVVADDKMAAFHAGLKR 240
Db 181 LRRKSPASQGMPCNVKAPLGSPPRRPRRAKRFASLSRFVETLVVADDKMAAFHAGLKR 240
Qy 241 YLLTWMAAAKAFKPSIRNPVSLVTRVLVILGSGEGPQVGSAAQTLSFCAMQRLN 300
Db 241 YLLTWMAAAKAFKPSIRNPVSLVTRVLVILGSGEGPQVGSAAQTLSFCAMQRLN 300
Qy 301 TPEDSDPHDFDTAILFTRODLGCVSTCDTLGMADVTVCDPARSCAIVEDDGLQSAFTAA 360
Db 301 TPEDSDPHDFDTAILFTRODLGCVSTCDTLGMADVTVCDPARSCAIVEDDGLQSAFTAA 360
Qy 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAVMAHVDPEEPWPCSFARFTTDFLDNGY 420
Db 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAVMAHVDPEEPWPCSFARFTTDFLDNGY 420
Qy 421 GHCLLDKPEAPLHLVPTFGKDYDADROCOLTFGPDSSRHCPLPPCAALWCSGHLNGHA 480
Db 421 GHCLLDKPEAPLHLVPTFGKDYDADROCOLTFGPDSSRHCPLPPCAALWCSGHLNGHA 480
Qy 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWPWGMDCSRTCCGGV 540
Db 481 MCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWPWGMDCSRTCCGGV 540
Qy 541 QFSRDCTRPVPRNGKYCEGRTRFRSCNTEDCPTGSALTFRBQCAAYNHRITDLFKSF 600
Db 541 QFSRDCTRPVPRNGKYCEGRTRFRSCNTEDCPTGSALTFRBQCAAYNHRITDLFKSF 600
Qy 601 PGPMWVPRYTGVAPODQCKLTCQARALGYVYVLEPRVVDGTPCSPDSSSVCQGRCHIA 660
Db 601 PGPMWVPRYTGVAPODQCKLTCQARALGYVYVLEPRVVDGTPCSPDSSSVCQGRCHIA 660
Qy 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQGNP 720
Db 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQGNP 720
Qy 721 GHSIYLAALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSGHGPLAQP 780
Db 721 GHSIYLAALKLPDGSYALNGEYTLMPSPDVLPGAVSLRYSGATAASETLSGHGPLAQP 780
Qy 781 LTLQVLVAGNPQDTRLRYSPFVPRPTPTPQDMLHRRQAIILEILRRRPWAGRK 837
Db 781 LTLQVLVAGNPQDTRLRYSPFVPRPTPTPQDMLHRRQAIILEILRRRPWAGRK 837
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RESULT 11
US-10-174-581-352
; Sequence 352, Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C41
; CURRENT APPLICATION NUMBER: US/10/174,581
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
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; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
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; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
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; PRIOR APPLICATION NUMBER: 60/063544
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; PRIOR FILING DATE: 1997-10-31
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; PRIOR FILING DATE: 1997-11-13
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; PRIOR APPLICATION NUMBER: 60/066466
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069425
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: 60/069870
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/068017
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
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; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
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; PRIOR APPLICATION NUMBER: 60/082704
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; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
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; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
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; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086023
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086486
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087098
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087208
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759

Query Match 99.8%; Score 4563; DB 14; Length 837;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSQTGSHPGRLAGRWLWGAQPCLLPIVPLSWLWLLLLASLLPSARLASPLPREEE 60
DB 1 MSQTGSHPGRLAGRWLWGAQPCLLPIVPLSWLWLLLLASLLPSARLASPLPREEE 60

QY 61 IVPEKLGSLVPGSGAPARLLCRLQAFGETLLLEQDSGVQVEGLTVQYLQAPPELLG 120
DB 61 IVPEKLGSLVPGSGAPARLLCRLQAFGETLLLEQDSGVQVEGLTVQYLQAPPELLG 120

QY 121 GAEPTGYLTGTINGDPESVASLHWDGGLIQLVQYRGAEHLQPLEGGTPNSAGPGGAI 180
DB 121 GAEPTGYLTGTINGDPESVASLHWDGGLIQLVQYRGAEHLQPLEGGTPNSAGPGGAI 180

QY 181 LRRKSPASGQGMVNCVAPKPLGSPSPRRRAKRFASLSRFVETLVVADDDKMAAFHGAGLKR 240
DB 181 LRRKSPASGQGMVNCVAPKPLGSPSPRRRAKRFASLSRFVETLVVADDDKMAAFHGAGLKR 240

QY 241 YLLTWMAAAKAFKHPISIRNPVSLVTRVLVILGSGEGPQVGPSSAAQTLSRFCAWQGLN 300
DB 241 YLLTWMAAAKAFKHPISIRNPVSLVTRVLVILGSGEGPQVGPSSAAQTLSRFCAWQGLN 300

QY 301 TPEDSDPDHFDTAILFTRODLGCVSTCDTLGMADVGTVCDDPARSCAIVEDDDGLQSAFTAA 360
DB 301 TPEDSDPDHFDTAILFTRODLGCVSTCDTLGMADVGTVCDDPARSCAIVEDDDGLQSAFTAA 360

QY 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAVMAHVDPPEPSPCSARFITTDFLDNGY 420
DB 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAVMAHVDPPEPSPCSARFITTDFLDNGY 420

QY 421 GHCLLDKPEAPLHLVPTFPKDYDADRCQQLTFGPDSDRHCPLPPPPCAALWCSGHLNGHA 480
DB 421 GHCLLDKPEAPLHLVPTFPKDYDADRCQQLTFGPDSDRHCPLPPPPCAALWCSGHLNGHA 480

QY 481 MCQTKHSPWADGTPCGPAQAACWGRCLHMDQLQDFNIPOAGGWPWGPWGDSCRTCCGV 540
DB 481 MCQTKHSPWADGTPCGPAQAACWGRCLHMDQLQDFNIPOAGGWPWGPWGDSCRTCCGV 540

QY 541 QFSRDCRTRVPRNGGKCEGRTRFRSCNTDCPTGSALTFRBEOCAAYNHRTDLFKSF 600
DB 541 QFSRDCRTRVPRNGGKCEGRTRFRSCNTDCPTGSALTFRBEOCAAYNHRTDLFKSF 600

QY 601 PGMDWVPRYTGVAPODQCKLTCQARALGYVYVLEPRVVDGTPCSPDSSVVCVQGRCIHA 660
DB 601 PGMDWVPRYTGVAPODQCKLTCQARALGYVYVLEPRVVDGTPCSPDSSVVCVQGRCIHA 660

QY 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGFRKFRYGYNNVVTIPAGATHILVROQGNP 720
DB 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGFRKFRYGYNNVVTIPAGATHILVROQGNP 720

QY 721 GHRISYIALKLPDGSYALNGEYTLMPSTPDVVLPGAVALRYSGATAASETLSHGHPLAQP 780
DB 721 GHRISYIALKLPDGSYALNGEYTLMPSTPDVVLPGAVALRYSGATAASETLSHGHPLAQP 780

QY 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPTPODLHRRRAQILLEILRRRPWAGRK 837
DB 781 LTLQVLVAGNPQDTRLRYSFVPRPTPTPTPTPODLHRRRAQILLEILRRRPWAGRK 837

RESULT 13
US-10-176-749-352
; Sequence 352, Application US/10176749
; Publication No. US20030017542A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C76
; CURRENT APPLICATION NUMBER: US/10/176,749
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 352
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-749-352

Query Match 99.8%; Score 4563; DB 14; Length 837;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSQTGSHPGRLAGRWLWGAQPCLLPIVPLSWLWLLLLASLLPSARLASPLPREEE 60
DB 1 MSQTGSHPGRLAGRWLWGAQPCLLPIVPLSWLWLLLLASLLPSARLASPLPREEE 60

QY 61 IVPEKLGSLVPGSGAPARLLCRLQAFGETLLLEQDSGVQVEGLTVQYLQAPPELLG 120
DB 61 IVPEKLGSLVPGSGAPARLLCRLQAFGETLLLEQDSGVQVEGLTVQYLQAPPELLG 120

QY 121 GAEPTGYLTGTINGDPESVASLHWDGGLIQLVQYRGAEHLQPLEGGTPNSAGPGGAI 180
DB 121 GAEPTGYLTGTINGDPESVASLHWDGGLIQLVQYRGAEHLQPLEGGTPNSAGPGGAI 180

QY 181 LRRKSPASGQGMVNCVAPKPLGSPSPRRRAKRFASLSRFVETLVVADDDKMAAFHGAGLKR 240
DB 181 LRRKSPASGQGMVNCVAPKPLGSPSPRRRAKRFASLSRFVETLVVADDDKMAAFHGAGLKR 240

QY 241 YLLTWMAAAKAFKHPISIRNPVSLVTRVLVILGSGEGPQVGPSSAAQTLSRFCAWQGLN 300
DB 241 YLLTWMAAAKAFKHPISIRNPVSLVTRVLVILGSGEGPQVGPSSAAQTLSRFCAWQGLN 300

QY 301 TPEDSDPDHFDTAILFTRODLGCVSTCDTLGMADVGTVCDDPARSCAIVEDDDGLQSAFTAA 360
DB 301 TPEDSDPDHFDTAILFTRODLGCVSTCDTLGMADVGTVCDDPARSCAIVEDDDGLQSAFTAA 360

QY 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAVMAHVDPPEPSPCSARFITTDFLDNGY 420
DB 361 HELGHVFNMLHNSKPCISLNGPLSTSRHVMAVMAHVDPPEPSPCSARFITTDFLDNGY 420

QY 421 GHCLLDKPEAPLHLVPTFPKDYDADRCQQLTFGPDSDRHCPLPPPPCAALWCSGHLNGHA 480
DB 421 GHCLLDKPEAPLHLVPTFPKDYDADRCQQLTFGPDSDRHCPLPPPPCAALWCSGHLNGHA 480

QY 481 MCQTKHSPWADGTPCGPAQAACWGRCLHMDQLQDFNIPOAGGWPWGPWGDSCRTCCGV 540
DB 481 MCQTKHSPWADGTPCGPAQAACWGRCLHMDQLQDFNIPOAGGWPWGPWGDSCRTCCGV 540

QY 541 QFSRDCRTRVPRNGGKCEGRTRFRSCNTDCPTGSALTFRBEOCAAYNHRTDLFKSF 600
DB 541 QFSRDCRTRVPRNGGKCEGRTRFRSCNTDCPTGSALTFRBEOCAAYNHRTDLFKSF 600

QY 601 PGMDWVPRYTGVAPODQCKLTCQARALGYVYVLEPRVVDGTPCSPDSSVVCVQGRCIHA 660
DB 601 PGMDWVPRYTGVAPODQCKLTCQARALGYVYVLEPRVVDGTPCSPDSSVVCVQGRCIHA 660

QY 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGFRKFRYGYNNVVTIPAGATHILVROQGNP 720
DB 661 GCDRIIGSKKFKDKCMVCGDGGSGCSKQSGFRKFRYGYNNVVTIPAGATHILVROQGNP 720

QY 721 GHRISYIALKLPDGSYALNGEYTLMPSTPDVVLPGAVALRYSGATAASETLSHGHPLAQP 780
DB 721 GHRISYIALKLPDGSYALNGEYTLMPSTPDVVLPGAVALRYSGATAASETLSHGHPLAQP 780

Db	241	YLLTVMAAAKAFKPSIRNPVSLVTVTRVLVILSGSEEGPQVGPFAAQTLRSFCAWORGLN	300
Qy	301	TPEDSPDHFDTAILFTRODLGCVSTCDTLGMADVTCVCDPARSCAIVEDDGLQSAFTAA	360
Db	301	TPEDSGPDHFDTAILFTRODLGCVSTCDTLGMADVTCVCDPARSCAIVEDDGLQSAFTAA	360
Qy	361	HELGHVFNMLHDSKFCISLNGPLSTSRHVMAVPMVAHVDPPEFPWSPCSARFITDFLDNGY	420
Db	361	HELGHVFNMLHDSKFCISLNGPLSTSRHVMAVPMVAHVDPPEFPWSPCSARFITDFLDNGY	420
Qy	421	GHCLLDKPEAPLHLPVTFPGKYDADROCOLTFGPDSSRHCPOLPPECAALWCSGHLNGHA	480
Db	421	GHCLLDKPEAPLHLPVTFPGKYDADROCOLTFGPDSSRHCPOLPPECAALWCSGHLNGHA	480
Qy	481	MCOTKHSFWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWGMPWPGDCSRTCGGV	540
Db	481	MCOTKHSFWADGTPCGPAQACMGRCCLHMDQLQDFNIPOAGGWGMPWPGDCSRTCGGV	540
Qy	541	QFSSRDCTRPVPRNGGKYCEGRTRFRSCNTEDCPTGSALTFRBOCAAYNHRTDLFKSF	600
Db	541	QFSSRDCTRPVPRNGGKYCEGRTRFRSCNTEDCPTGSALTFRBOCAAYNHRTDLFKSF	600
Qy	601	PGMDWVPRTGYAPODOCKLTCOARALGYVYVLEPRVVDGTPCSPDSSVVCQGRCIHA	660
Db	601	PGMDWVPRTGYAPODOCKLTCOARALGYVYVLEPRVVDGTPCSPDSSVVCQGRCIHA	660
Qy	661	GCDEIIGSKKKFKDKMVCGGDGGSGCSKQSGSFRKFRYGYNVVTIPAGATHILVROQGNP	720
Db	661	GCDEIIGSKKKFKDKMVCGGDGGSGCSKQSGSFRKFRYGYNVVTIPAGATHILVROQGNP	720
Qy	721	GHRSIYLALXLPDGSYALNGEYTLMPSPDVLPGAVLSRYSGATAASETLSCGHGLAQP	780
Db	721	GHRSIYLALXLPDGSYALNGEYTLMPSPDVLPGAVLSRYSGATAASETLSCGHGLAQP	780
Qy	781	LTLOVLVAGNPQDTRLRYSPFVPRPTPTPRTPQDMLHRRRAQILEILRRRPWAGRK	837
Db	781	LTLOVLVAGNPQDTRLRYSPFVPRPTPTPRTPQDMLHRRRAQILEILRRRPWAGRK	837

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 12:42:07 ; Search time 51 Seconds
(without alignments)
1579.087 Million cell updates/sec

Title: US-09-634-287E-2
Perfect score: 4570
Sequence: 1 MSQTSHPGRLAGRWLGA.....LHRAQILEILRRPWAQRK 837
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4566	99.9	837	T00355	hypothetical prote
2	2158	47.2	951	T00017	gene ADAMTS-1 prot
3	1375.5	30.1	550	T47158	hypothetical prote
4	1317	28.8	1205	T21371	hypothetical prote
5	950.5	20.8	1205	T18517	procollagen N-endo
6	480.5	10.5	1558	C89114	protein C37C3.6a (
7	480.5	10.5	2167	T34395	hypothetical prote
8	415.5	9.1	1444	T18856	angiogenesis inhib
9	389	8.5	860	T18892	hypothetical prote
10	365	8.0	951	T00260	hypothetical prote
11	313	6.8	903	S60257	meltrin alpha - mo
12	284.5	6.2	957	T15976	hypothetical prote
13	268.5	5.9	609	S55270	catracoilaatin p
14	268.5	5.9	814	G02390	disintegrin-like m
15	267	5.8	616	A55796	ecarin precursor -
16	266.5	5.8	1170	1 TSHUP1	thrombospondin 1 p
17	263.5	5.8	1059	T22545	hypothetical prote
18	263	5.8	1170	A40558	thrombospondin 1 p
19	260	5.7	571	S24789	jararhagin C precu
20	253	5.5	480	A30065	trigraamin precurs
21	231	5.5	1178	A39804	thrombospondin pre
22	250	5.5	419	S41607	atrolysin A (EC 3.
23	243	5.3	478	A43296	atrolysin E (EC 3.
24	241.5	5.3	610	JC7530	vascular apoptosis
25	239.5	5.2	407	S66260	metalloproteinase
26	239.5	5.2	549	S48169	metalloproteinase
27	237.5	5.2	826	A60385	monocyte surface a
28	237.5	5.2	1172	1 TSHUP2	thrombospondin 2 p
29	235.5	5.2	478	JC4880	fibrinolytic metal

30	234.5	5.1	617	2	S48160	metalloproteinase
31	233.5	5.1	469	1	S29126	properdin precursor
32	231	5.1	478	2	JQ1301	hemorrhagic protei
33	229	5.0	655	2	JC7850	disintegrin and me
34	228.5	5.0	1172	2	A42587	thrombospondin 2 p
35	227.5	5.0	429	2	A42972	coagulation factor
36	227.5	5.0	481	2	JC4342	fibrinolytic prote
37	225.5	4.9	481	2	S43125	trifimucin precursor
38	225	4.9	508	2	T22836	hypothetical prote
39	223.5	4.9	610	2	JC8056	halyase - Glycidu
40	221.5	4.8	952	2	T18900	disintegrin and me
41	217.5	4.8	414	1	HYRSAC	atrolysin C (EC 3.
42	217.5	4.8	1074	2	JC5928	semaphorin F precu
43	216.5	4.7	1042	2	T26644	hypothetical prote
44	214.5	4.7	411	1	HYSNFA	fibrolase (EC 3.4.
45	213.5	4.7	414	2	S41609	atrolysin C (EC 3.

ALIGNMENTS

RESULT 1

T00355
hypothetical protein KIAA0688 - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C:Accession: T00355
R:Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.,
DNA Res. 5, 169-176, 1998
A:Title: Prediction of the coding sequences of unidentified human genes. X. The complete
A:Reference number: Z14142; MUID:98403880; PMID:9734811
A:Accession: T00355
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-837 <ISH>
A:Cross-references: UNIPROT:O75173; EMBL:AB014588; NID:G3327189; PIDN:BAA31663.1; PID:G3;
A:Experimental source: brain
C:Genetics:
A:Gene: KIAA0688
P:519-575/Domain: thrombospondin type 1 repeat homology <THR3>

Query Match 99.9%; Score 4566; DB 2; Length 837;

Best Local Similarity 99.9%; Pred. No. 1.8e-302;

Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MSQTSHPGRLAGRWLGAQPCLLPIVPLSWLWLLLLASLPSARLASPLPREE	60
DB	1	MSQTSHPGRLAGRWLGAQPCLLPIVPLSWLWLLLLASLPSARLASPLPREE	60
QY	61	IVFPEKLNGSVLPGSGAPARLCRLQAQFETLLLEQDSGVQVEGLTVQYLQAPPELLG	120
DB	61	IVFPEKLNGSVLPGSGTAPARLCRLQAQFETLLLEQDSGVQVEGLTVQYLQAPPELLG	120
QY	121	GAEPTTYLTGTINGDPESVASLHWDGGALLGVQVRGAELHLOPLEGGTPNSAGGPAHI	180
DB	121	GAEPTTYLTGTINGDPESVASLHWDGGALLGVQVRGAELHLOPLEGGTPNSAGGPAHI	180
QY	181	LRKPSAQSGQPMCNVKAPLGSPSPRRRAKFAFASISREVTLVVADDDKMAAFHAGLKR	240
DB	181	LRKPSAQSGQPMCNVKAPLGSPSPRRRAKFAFASISREVTLVVADDDKMAAFHAGLKR	240
QY	241	YLLTWMAAAKAFKHPISRNPNVSLVRLVILGSGEGPQVGPSPAAQTLSFCAMORGLN	300
DB	241	YLLTWMAAAKAFKHPISRNPNVSLVRLVILGSGEGPQVGPSPAAQTLSFCAMORGLN	300
QY	301	TPEDSDPHDFTAILFTTRQDLGCVSTCDTLGMADVTGTCDPARSCAIVEDDGLQSAFTAA	360
DB	301	TPEDSDPHDFTAILFTTRQDLGCVSTCDTLGMADVTGTCDPARSCAIVEDDGLQSAFTAA	360
QY	361	HELGHVFNMLHDNSKPCISLNGPLSTSHVMAVMAHVDPPEPSPCSARFITDFLDNGY	420
DB	361	HELGHVFNMLHDNSKPCISLNGPLSTSHVMAVMAHVDPPEPSPCSARFITDFLDNGY	420

[illegible]

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792 DDICVAGACWPAGCDHQJHSTLRDRDKCVCGDDSSCKVVGKTFNEQGTFGVNEVWKIFA 791
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798 GATHILVRQOG--NPGHRSYI LALKLPDGSYALNGEYTLMPSPDVLVLPFGAVSLRYSYGAT 765
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00022; CESP:F22

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T18517
procollagen N-endopeptidase (EC 3.4.24.14) I - bovine
N;Alternate names: procollagen N-proteinase
C;Species: Bos primigenius taurus (cattle)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18517
R;Colige, A.; Nusgens, B.V.; Lapiere, C.M.
submitted to the EMBL Data Library, February 1996
A;Description: Cloning of the cDNA of the bovine procollagen I N-proteinase.
A;Reference number: Z18941
A;Accession: T18517
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1205 <COL>
A;Cross-references: UNIPROT:P79331; EMBL:X96389; NID:e90769; PID:e228215; PDB:
A;Experimental source: skin
C;Genetics:
A;Gene: PC I-NP
C;Function:
A;Description: catalyzes cleavage of the propeptides of type I and II collagen
C;Keywords: hydrolase; metalloproteinase

Query Match      20.8%; Score 950.5; DB 2; Length 1205;
Best Local Similarity 31.8%; Pred.No.1.6e-56;
Matches 282; Conservative 119; Mismatches 334; Indels 153; Gaps 42

QY      8  PGRGLAGRWLWGAQPCILLITPIVLSWLWLLLLLLASLLPSARLASPLP-----R 57
Db      3  PPAGNAGR-----LLCPA-----LLLLLLLLPLPADARLAAAAADPPGPGQHGA 46

QY      58  EEEIVFP-----EKLNSVLPGGSGAPA-----RLLCRIQ 86
Db      47  ERILAVPVRTDAQGRLVSHVVSAATAPAGVTRRAAPAIPLSGSGSEDPGGRIFYNYT 106

QY      87  AFGETLLLELEQDSGVQVEGLTYQYLGAPELLGGA---EP--CTYL--TGTING--DPES 138
Db      107  VFGRDLHLRLRPNARLVAPATVEWQGES-----GATRVPELLGTCLYXVDVAGLAESS 161

QY      139  VASLHWPGGALLGLVLYVRGAEHLHPILEGGTPNSAGGPG-AHLIRKKGPSAGOGPMCNVK 197

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Qy	519	QAGWGPWGPCSRTCCGGVQFSSRDCTRPVPRNGKVCGRRTFRSCNTDCPTGS	578
Db	75	ETGNGWGPWPCNSRSRSCGGVQLEKRCQSGD-----CTGASVRYISCNLNACESGT	126
Qy	579	ALTFREBOCAAYNHRITDLFKSFPQPM-----WVPRYTGVAPQDQCKLTQCARALGYVYV	633
Db	127	--DFRAEQCKFNDEA-----LDGNYHKWTP-YKG---KNKCELVCKPESGNFYK	171
Qy	634	LEPRVVDGTPCSPDSSVQVQRCIIHAGCDRIIGSKKPKCMVCGDGGSCSKQSGSF-	692
Db	172	WADKVVVDGTKCDKSKNDICVDGCLPVGCDGKGLSLKFDKCKGCDGCTCTKTIERFD	231
Qy	693	-RKFRYGVNNVVTIPAGATHILVRQGNPGHRSIYLALKLPDGSYALNGEYITLMPSTDV	751
Db	232	ERNLSPGYHDIILKPEGATNIKIOEARKSTNN---LALKNGSDHFLYNGN-GLIQVEKEV	287
Qy	752	VLPGAVSLRYSGATASETLSHGHPLAQPLTLQVLVAGNPQDTRLRYSFVFP	803
Db	288	EVGGTI---FVYDDAEPTLSAQGLSELTALLFRKSRDTAIKYEFSIP	336
RESULT 7			
T34395			
hypoetical protein C37C3.6b - Caenorhabditis elegans			
C:Species: Caenorhabditis elegans			
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004			
C:Accession: T34395; T34394			
R:Geisel, C.; Bradshaw, H.			
A:Description: The sequence of C. elegans cosmid C37C3.			
A:Reference number: Z21518			
A:Accession: T34395			
A:Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: DNA			
A:Residues: 1-2167 <GSI>			
A:Cross-references: UNIPROT:076840; EMBL:U64857; PIDN:AAC25868.1; GSPDB:GN00023; CESP:C37C3			
A:Experimental source: strain Bristol N2; clone C37C3			
A:Accession: T34394			
A:Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: DNA			
A:Residues: 1-1555, 'SKF' <GE2>			
A:Cross-references: EMBL:U64857; PIDN:AAC25867.1; GSPDB:GN00023; CESP:C37C3.6a			
A:Experimental source: strain Bristol N2; clone C37C3			
C:Genetics:			
A:Gene: CESP:C37C3.6b; CESP:C37C3.6a			
A:Map position: 5			
A:Introns: 32/3; 104/2; 156/2; 207/1; 459/2; 536/3; 577/2; 1105/3; 1367/1; 1438/1; 1556/1			
Query Match 10.5%; Score 480.5; DB 2; Length 2167;			
Best Local Similarity 35.6%; Pred. No. 2.7e-24; Indels 37; Gaps 10;			
Matches 104; Conservative 46; Mismatches 105;			
Qy	519	QAGWGPWGPCSRTCCGGVQFSSRDCTRPVPRNGKVCGRRTFRSCNTDCPTGS	578
Db	75	ETGNGWGPWPCNSRSRSCGGVQLEKRCQSGD-----CTGASVRYISCNLNACESGT	126
Qy	579	ALTFREBOCAAYNHRITDLFKSFPQPM-----WVPRYTGVAPQDQCKLTQCARALGYVYV	633
Db	127	--DFRAEQCKFNDEA-----LDGNYHKWTP-YKG---KNKCELVCKPESGNFYK	171
Qy	634	LEPRVVDGTPCSPDSSVQVQRCIIHAGCDRIIGSKKPKCMVCGDGGSCSKQSGSF-	692
Db	172	WADKVVVDGTKCDKSKNDICVDGCLPVGCDGKGLSLKFDKCKGCDGCTCTKTIERFD	231
Qy	693	-RKFRYGVNNVVTIPAGATHILVRQGNPGHRSIYLALKLPDGSYALNGEYITLMPSTDV	751
Db	232	ERNLSPGYHDIILKPEGATNIKIOEARKSTNN---LALKNGSDHFLYNGN-GLIQVEKEV	287
Qy	752	VLPGAVSLRYSGATASETLSHGHPLAQPLTLQVLVAGNPQDTRLRYSFVFP	803
Db	288	EVGGTI---FVYDDAEPTLSAQGLSELTALLFRKSRDTAIKYEFSIP	336
Query Match 10.5%; Score 480.5; DB 2; Length 1558;			
Best Local Similarity 35.6%; Pred. No. 1.9e-24; Indels 37; Gaps 10;			
Matches 104; Conservative 46; Mismatches 105;			
Db	162	VALNSCDG--LAGLIRMEERFIEPLEKGLAAKEAQGRVHVYH-PTTSRPP-----	213
Qy	198	APLGSP-----SPRPRKGFASLSRFVETLVVADDKM	230
Db	214	-PLGGPOALDTGISADSLDLSRALGVLEBVRVNSSRRRRRAADDDYNIIEVLGVDDSV	272
Qy	231	AAFHGA-GLKRYLLTMAAAAFKHPSTRNPSVLVTVTLVILSGECP--QVGFSAQA	287
Db	273	VQPHGTEHVOKYLLTLNINVEIYHDESIGAHINVLVRIILLSYKMSLSIEIG-NPSQ	331
Qy	288	TLRSFCAWRGRLNTPSDSDPHDFTAILFTFRLQDLCGVSTCDTLGMADVGTGCDPARSAI	347
Db	332	SLENCWAYLQKPTDDEYHDHAI FLTRQDF-GPSGMQ--GYAPVTGMCHPVRSCITL	388
Qy	348	VEDDGLQSAFTAHEIGHVFNMLHD-NSKPCISLNGPLSTSRHVMAFMAHVDPEEPWSP	406
Db	389	NHEDGFSFAFVAHETGHVLMGHEHDQGNRC-----GDEVRLGSIAPLVAQAAHFRHWSR	444
Qy	407	CSARFTDFLDNGVGHCLLDKP---EAPLHLPTVFPKDYDADRCQLTFGPDSSRCPQL	463
Db	445	CSQQLSRYL-HSY-DCLRDPTFDWPA-LP-QLEGLHYSMNEQCRDFGLGYMMCTAF	500
Qy	464	P--PPCAALWCSHGLHGHAMCOTKHSPWADGTPCGPAQACMGGRCLHM--DQLODFNIPQ	519
Db	501	RTFDECKQLWCS-HPDNPYFCKTKKGPPLDGTMCAPGKHCFCGHCILWLPDILK-----R	554
Qy	520	AGWGPWGPCSRTCCGGVQFSSRDCTRPVPRNGKVCGRRTFRSCNTDCPTGS	579
Db	555	DGNWGAWSPPGSCSCTGTVKTRQCDNPNHANGRTCSGLAYDFOLCNSQDCFDALA	614
Qy	580	LTFRBOCAAYNHRITDL-FKSFPQPMDWVPRYTGVAPQDQCKLTQCARALGYVYVLEPRV	638
Db	615	-DFREBOCAAYNHRITDL-FKSFPQPMDWVPRYTGVAPQDQCKLTQCARALGYVYVLEPRV	668
Qy	639	VDGTPCS-PPSSSVQVQRCIIHAGCDRIIGSKKPKCMVCGDGGSCSKQSGSFKE--	695
Db	669	HDGTRCSYKDAFSLCVRGDCRKGCVGIVGSSQEDKCGVCGGNDGSHCKVKGTFGRSPK	728
Qy	696	RYGVNNVVTIPAGATHILVRQGNPGHRSIYLALK-LPDGSYALNGEYITLMPSTDVLP	754
Db	729	KLGIKWEIPAGARHLLIQEADTTSH--HLAVKNLETGKFLINEENDVDPNSTKPIAM	785
Qy	755	GAVALRYSGATASETLSHGHPLAQPLTLQVLVAGNPQDTRLRYSFVFP	802
Db	786	G-VEWEYRDED-GRETLQTMGLHGTITVLVIPEGDAR-ISLTYKIMI	830
RESULT 6			
C89114			
protein C37C3.6a [imported] - Caenorhabditis elegans			
C:Species: Caenorhabditis elegans			
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004			
C:Accession: C89114			
R:Anonymous, The C. elegans Sequencing Consortium.			
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog			
A:Reference number: A75000; MUID:99069613; PMID:9851916			
A:Note: see websites genome.wustl.edu/gsc/c_elegans/ and www.sanger.ac.uk/Projects/C_ele			
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and			
A:Accession: C89114			
A:Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1-1558 <STO>			
A:Cross-references: UNIPROT:Q81710; GB:chr_V; PIDN:AAC25867.1; PID:G3294501; GSPDB:GN000			
C:Genetics:			
A:Gene: C37C3.6a			
A:Map position: 5			
Query Match 10.5%; Score 480.5; DB 2; Length 1558;			
Best Local Similarity 35.6%; Pred. No. 1.9e-24; Indels 37; Gaps 10;			
Matches 104; Conservative 46; Mismatches 105;			

	Query March Best Local Similarity Matches 214;	6.8%; 22.7%; Conservative 103;	DB 2; Pred No. 2.4e-13; Mismatches 393;	Length. 903; Indels 234; Gaps 47;
QY	38	LLLLLASLLPSGARIASLPFREEEIVFPKLGNSVL-----PGSGAPAR-----	LLCRLO	86
DB	15	LLLLLAGALLAPRAARGMSLWDQRCAYEVARASLLSKDPGFGOSIPAKOHPDVLTVOLQ	74	
QY	87	AFGETLLELQDQSGVQVEGLT-VQYL--GQAPELLGGAEPGYTLTGTINGDPESVASLH	143	
DB	75	LESRDLIILSLERNEGLIANGFTETHYLQDGTSLTRNHTDHCYVGHVQGDAAASVVLSLS	134	
QY	144	WDGGALLGVLYQRGAEHLQPLEGGTPNSAGCGPAHILRRKPSAGSGGPMCNVKAPLGSP	203	
DB	135	-TCSDLRGLIMPENKTYGLEPMKNTTDSYKLVPAESMTNIIQGLCGSHQNSLNTWEDVSP	193	
QY	204	SPRPRRAKRF----ASLSRFVETLVVADKMAAFHGAGL----KRYLLTVMAAAAKAFKP	256	
DB	194	GTSQMRARRHKKRETLKMTKYVELVTIVADNRFFORQGDLEKVKQRLRIANHVDFKFR--	251	
QY	257	STRNPVSIWVTVRLVILG-----SGEEGPQVPSAAQTLSRFCAWORGLNTPEDSDPDHDT	312	

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Db 91 EKKGSLDFGSLDSD---CHYHYGKVAIAISGCDG-----RIVSESNRKQG-----135
QY 125 GTYLTGTINGDPDSVASLHWDGALLGVQYRGAELHQLPLEGTPNSAGGPGCAHLIRK 184
Db 136 -----KGTVIDDGEI-----IVVHPFDHHAHRKATEN-----GAHVYKR 173
QY 185 SPASGGQPMCNVKAPLGSPSPRRRAKRFASLRFVETLVVADDKMAAF-----233
Db 174 ETLAGE-----PKDFGLDNVVTESLVEDSAIFEDVPVTQRLT 214
QY 234 -----HGA-----GLKRYLLTMAAAAKAFKHPSPTRNPVSLV 265
Db 215 QQSDLIVELAVFDENLWRHFSSKHGGMADKLDQYTLTLNNIQTMYQTASPELTER 274
QY 266 VTRLVILSGEEGPQVG-----PSAAQTLSFCAWQGLNTPEDSPDHDFTAILTROD 320
Db 275 VIRYEVLTROPALAGYLHNHGAOMYLDRCRYORNLAVRD-----WDHAIMLTGYD 327
QY 321 L-CGVSTCDTLGMADVGTVCDPARSAIVEDDGLQSAFTAHAHELGHVFNMLHDNSKPCI- 378
Db 328 IHRGAGSRISGIALDGMCDPNTCTLAEGLDFTSAFETGHELGRFTELKDKHSDTLF 387
QY 379 --SLNGPLS-----TSRHMAPVMAHVDP-----EPPWS-----405
Db 388 TGTFCGSPKWCQLGRCVPMGTGTNEIQTVOHVAPVVTTLPSRIDGWSWGATICSQCTC 447
QY 406 -----PCSAPIITDFLNGYCHCLDKPEAPLHLPVTPGKYDADQOC-- 449
Db 448 NGILSVGLAIARTCSAPYA-----NGGSDCVGSTRAVL-----CSRQGR 491
QY 450 -----QLTFGPDSPHRCPLPPPCAALWCSHGLNHGAMQTKH 486
Db 492 ASKSVDYEISDKMEQKRLKNDRELT-GKGSQ-LNRFPPQACKVCD--VQHYGSGQRY 547
QY 487 SPWA-----DGTGCGPAQAACMGRCCLHMD-----QLQDFNIP-----OAGGW 523
Db 548 RFPGLDLPDGTSCGYDRYCLDGECLALNCNNALISRDQSCPTDTCPIITDQSSSVYRGOW 607
QY 524 GPMGPMGDCSRTCGGVQVFSRDCRTPVRNGGKYCEGRTRFRSCNTEDCPT-----576
Db 608 GTWSLTSTACTCGGTRKRNACST-----GQCEGNEDETEVCSSSPSLVRVGNB 661
QY 577 -----GSALTFRBQCAAYNHRITLDFKSPGPMDMWVPRYTGVAPODQCKLT 622
Db 662 WSTWTWNHCSVSCGRSQARYKCLS-PRITLAP-DCFG-----ENKVT 704
QY 623 COAR-----ALGYVYV-----LEPRVVDGTPCS-----PDSSS 650
Db 705 NELRITFFKARSYIMGSRVRCNKKIKRNTISEKNIEVASCNDGPNAGVMTGGMWSTCST 764
QY 651 VCVQV-----RCIHAGCDRIIGSKKFKDKMV--CGGDG-----SGCSKQSG 690
Db 765 SCGPGTLVRQRTCNREPCD---GSAHERRSCNVATCONDGWSLWNSWSDCSRVOG 817

RESULT 13
S55270
catrocollastatin precursor - western diamondback rattlesnake
C;Species: Crotalus atrox (western diamondback rattlesnake)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C;Accession: S55270
R;Zhou, Q.; Smith, J.B.; Grossman, M.H.
Biochem. J. 307, 411-417, 1995
A;Title: Molecular cloning and expression of catrocollastatin, a snake-venom protein from
A;Reference number: S55264; MUID:95251603; PMID:7733877
A;Accession: S55270
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-609 <H>
A;Title: Expression of members of a novel membrane linked metalloproteinase family (ADAM)
A;Cross-references: UNIPROT:Q90282; GB:U21003; NID:G710353; PIDN:AAC59672.1; PID:G710354
C;Superfamily: mouse meltrin alpha; disintegrin homology
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Query Match 5.9%; Score 268.5; DB 2; Length 609;
Best Local Similarity 23.1%; Pred. No. 1.6e-10;
Matches 161; Conservative 97; Mismatches 265; Indels 175; Gaps 38;

QY 37 ILLLLLASLLP-----SARLASPLPREEEIVFEKLNGSVLP-CSGAPA---RLLCRLQAF 88
Db 5 LVTICLAAPPYQGSIILESNVNDYEVYPRKV--TALPKGAVQPKYEDAMQYELKVN 62
QY 89 GETLLELQDQSGVQVVEGLTVQVL---GQAPELLGGAEPGTLYLTGTINGDPSPVASLHMD 145
Db 63 GEPVVLHGLKNGKLPKSDYSETHYSPDREITYPLVEDHCYHYHRIENDADSTAISAC 122
QY 146 GGALLGLVLYRGAELHQLPLEGTPNSAGGPGCAHLIRKSPASGQG---PMCNVKAPLGS 202
Db 123 NG-LKGHPKQLQEMYLIEPLK-LPDSE---AHAVKYENVEKEDEALKMCGVTQWES 175
QY 203 PSRPRRAKRFASLS-----RFVETLVVADDKMAAFHAGL---KRYLLTMAAAAKA 252
Db 176 YEPKIKASQLVVTAEHQKYNPFRFVELFLVVDKAMVTKNNGDLDKIKRMYEIVNTVNEI 235
QY 253 FKHPSTRNPVSLVTVRLVILSGEEGPQVPSAAQTLSRFCAMQRCGLNTPEDSDPHFDT 312
Db 236 YRYMYIH--VALVGLB---IWSNEDKITVYKPGYTLNAGFGEWK---TDLTRKKG-DN 286
QY 313 AILFTRQDLGCVSTCDTLGMADVGTVCDPARSAIVED---DGLQSAFTAHAHELGHVFN 369
Db 287 AQLLTAIDLDRV-----IGLAYVGSMPKPRSTGIIQDYSEINLVVAVIMAHMGHNLGI 341
QY 370 LHDNSKPCISLNGPLSTSRH--VMAPVMAHVDPPEPSPCSARFITDLDNGYGHCLLDK 427
Db 342 NHD-----SGYCSGCDYACIMRPEIS-PEPSTFSPNSCYFPCWDFIMNHNPECILNE 392
QY 428 PEAPLHLPVTEP-----GKYD--ADRCQLTFGPDSRHCPLPPPCAALWC---472
Db 393 ----PLGTDIISPPVCGNELLEVGEBCDCGTPENCQ-----NEC-----CDARATCKLK 436
QY 473 SGHLNHGAMC--QTKHSP-----WADGTPCGPAQAACMGRCCLHMDQLDQFNIPQAGWGP 525
Db 437 SGSQCGHGDCCEQCKFKSGTECRASMSCECDPAEHCTG-----474
QY 526 WGPWGDSCRTCGGVQVFSRDCRTPVRNGGKYCEGRTRFRSCNTEDCPT-----576
Db 475 -----QSSECPADVFNKNGQPC---LDNYGYCYNGNCPIMYHCYVDLF 514
QY 577 GSALTFRBQCAAYNHRITLDFKSPGPMDMWVPRYTG---VAPQD-QC-KLTQCAALG- 629
Db 515 GADVVEADESCFRNQKGNYY-----CYCKENGKIPCAPEDYKCGRLYCKDNSPGQ 567
QY 630 -----YYVLEPR-----VVDGTPCSPDSSSVQVQGRCI 658
Db 568 NNPCKMFYSNEDEHKGMLPGTKCA--DGKVCNSGHCV 603

RESULT 14
G02390
disintegrin-like metalloproteinase MDC15 (EC 3.4.24.-) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 31-Dec-2000
C;Accession: G02390; PC4263
R;Herren, B.; Raines, E.W.; Ross, R.
submitted to the EMBL Data Library, January 1996
A;Reference number: H01157
A;Accession: G02390
A;Status: preliminary; translated from GB/EMBL/DBDJB
A;Molecule type: mRNA
A;Residues: 1-814 <H>
A;Cross-references: EMBL:U46005; NID:g1335871; PIDN:AAC51112.1; PID:g1335872
R;McKie, N.; Edwards, T.; Dallas, D.J.; Houghton, A.; Stringer, B.; Graham, R.; Russell,
Biochem. Biophys. Res. Commun. 230, 335-339, 1997
A;Title: Expression of members of a novel membrane linked metalloproteinase family
A;Reference number: PC4263; MUID:97168971; PMID:9016778
A;Accession: PC4263
A;Status: nucleic acid sequence not shown
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A:Molecule type: mRNA
 A:Residues: 1-461 <MCK>
 A:Experimental source: articular chondrocyte
 C:Comment: This protein is a membrane bound protein and involved in cell/cell and cell/m
 C:Superfamily: mouse meltrin alpha; disintegrin homology
 C:Keywords: hydrolase; metalloproteinase; zinc
 F:420-503/Domain: disintegrin homology <DIS>
 F:348,352,358/Binding site: zinc (His) #status predicted
 F:349/Active site: Glu #status predicted

Query Match 5.9%; Score 268.5; DB 2; Length 814;
 Best Local Similarity 24.3%; Pred. No. 2.2e-10;
 Matches 187; Conservative 82; Mismatches 259; Indels 243; Gaps 45;
 QY 34 LVLMLLLLA-SLLPSARLASPLPR-----EEIVFPEKINGSVLPG-----74
 DB 5 LLMALGLLNGSPFS-----WPLPNIGTTEEQAESEKAPREPLEPQVLDLPLSLKKV 60
 QY 75 --SGAPARLLCRIOAFGETLLLEQD-----SGVOV--EGLTVQYLQQA 115
 DB 61 LQTSLEPLRIKLELDGDHSHLELQNLRELVPGRPTLVWYQPDGTRVSEGHTELCYQ 120
 QY 116 PELLGGAPEPTY-----LTCINGDPESVASLHWDGGLLIG-VLQVRGAELHLQPLE 166
 DB 121 GRVRGYA--GSWSICTCSGLRGLVLTTPERSVTLQPGDLOGPPIISRIQDLHLP--- 175
 QY 167 GGTGPSAGGPGCAHLIRKSPASGGGPMCNVKAFLGSPSPRRPRRAKRFASLSRVEVLVVA 226
 DB 176 -----GHTCALSWESEVHTQTP-----EHLPGQRHRRRR--DVWTETKTVELVIVA 221
 QY 227 DDKMAAFHAGLRYLLTVMAAAKAFKPSIRN-PVSLV-----TRVLIG--- 273
 DB 222 DHSEA-----QKY-----RDFHLNRLTLEVALLLDFFRPLNVRVALGLEAW 265
 QY 274 SGEFGVGPSSAOTLRSFCAWORGLNTPEDSDPDHPTAILFTRODLQGVSTCDTLGMA 333
 DB 266 TQRLVELSPNPAVTLNFWRAHLLPLP-----HDSALVTGTSFSG-----PTVGMA 317
 QY 334 DVGTVCDPARSCAIVEDG---LQSAFTAHELGHVFNMLHD---NSKPCISLNGPLSTS 387
 DB 318 IONSICSPDFSGGVNMDHSTSLGVASSIAHELGHSLGLDHLDFGNSCPC---PGPAPAK 374
 QY 388 RHVAPVMAHYD--PEEPWSPCSARFTDFLDNGYGHCLLDK-PEAPLHLPV-TFPGKDY 443
 DB 375 TCIME---ASTDFLPLNFSNCSRALEKALLDNGSCLFERLPSLP---PMAAFCGNMF 428
 QY 444 -DADRQCOLTFGPSRHCPLPPPCAALWCSCGHLNGHAM-----CQTKHSPW----- 489
 DB 429 VEPGEQCDGFLDD---C--VDPCCDSLTCQLRPGAQACASDGPCCQNCOLRPSGWQCRPT 483
 QY 490 -----ADGTPCGPAQA-CWGGRCI-HMDOLQDFNIPQAGGWG 524
 DB 484 RQCDLPEFCDSQCPDPSVSLGDGECAGGQAVCMHGRCASTAQCCSL----- 534
 QY 525 PWGPMGDCSRCTGGGVQFSSRDCTPVPVRNGGKYCEGRTRFRSCNTEDCPTGS--ALTF 582
 DB 535 -WGP-----GAQPAAPLCIQTANTRG-----NAFGSGGRN--PSGSYVSCPT 573
 QY 583 REEQCAAYNHRITDLFKSPFGPM-----DWVPRYTVAPQDCKLTCQA 625
 DB 574 RDAICGQLOQCQGTQRTQPLIGSIRDLLWETIDVNGTELNCSSWVHLDLG---SD----- 622
 QY 626 RALGYVYVLEPRV-VDTGTPCSPDSSVCVQGRCIHAGCDRIIGSKKFKDKC 675
 DB 623 -----VAQPLLLTLPGTACGP--GLVCIDHRCQRVD---LLGAQECRSKC 661

RESULT 15
 A55796
 ecarin precursor - saw-scaled viper
 C:Species: Echis carinatus (saw-scaled viper)
 C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
 C:Accession: A55796

R:Nishida, S.; Fujita, T.; Kohno, N.; Atoda, H.; Morita, T.; Takeya, H.; Kido, I.; Paine,
 Biochemistry 34, 1771-1778, 1995
 A:Title: cDNA cloning and deduced amino acid sequence of prothrombin activator (ecarin) f
 A:Reference number: A55796; MUID:95151760; PMID:7849037
 A:Accession: A55796
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-616 <NIS>
 A:Cross-references: UNIPROT:Q90495; GB:D32212; NID:g717090; PIDN:BAA06910.1; PID:g717091
 C:Superfamily: mouse meltrin alpha; disintegrin homology
 F:404-486/Domain: disintegrin homology <DIS>
 F:338/Active site: Glu #status predicted

Query Match 5.8%; Score 267; DB 2; Length 616;
 Best Local Similarity 22.9%; Pred. No. 2e-10;
 Matches 161; Conservative 85; Mismatches 279; Indels 178; Gaps 37;
 QY 37 LLLLLLASLLP-----SARLASPLPREBEIVPEKINGSVLPGSAPAR-----LLCR 84
 DB 5 LLLVILCLAVFPVQGCIIILGSGNVNDYVVPQKV--TALP-KGAVQOQPEQKYEDAMOYE 61
 QY 85 LQAFGETLLLEQDSGVQVVEGLT-VQYLGOAPELL--GGAEPGTYLGTGTGDPESVAS 141
 DB 62 FEVKGEPVVLHLEKNKELFSEYSETHYSSDDREITNPVSVEDHCYHGRIONDAESTAS 121
 QY 142 LHWDCGALLGVQVRGAELHLQPLEGGTPNSAGPGGAHLIRKSPASGQG---PWCNV-- 196
 DB 122 ISACNG-LKGFHKLGETYFIEPLK--IPDSE---AHAVKYENIENEDEAPKMGCVTQ 174
 QY 197 -----KAPLGSPSPRRRAKRFASLSRFEVTLVADDKMAAFH---GAGLKRYLLT 244
 DB 175 DNWSEDEPKTKTLGLIVPHER--KFE--KKFIELVVVVVDHSMVTYKNNDSSTAIRTYIE 230
 QY 245 VMAAAKAFKPSIRNPVSLVTVLVLGSGEGVQVPSAAQTILRSFCAMQWG---LNTPT 302
 DB 231 MLNTVNEIYLPNIR--VALVGLFEWNG---DLINVTSTADDTLHSGEWRASLLNR- 284
 QY 303 EDSDDPHFDTAILFTRODLQGVSTCDTLGMADVGVCDPARSCAIVEDG---LOSFTA 359
 DB 285 -----KRHDHAQLLNTVTL---DHSTLGITFVYGMCKSDRSVELILDYSNITFNMAVII 335
 QY 360 AHELGHVFNMLHD-----NSKPCISLNGPLSTRHVMAPVMAHYDPEEPWSPCSARFT 413
 DB 336 AHMGHSLGMLHDTKFTCTGAKPCINFG-----KESIPPPKEFSSCSYDQYN 382
 QY 414 DFLDNGYGHCLLDKP-EAPLHLPVTFPGKDYADACQQLTFGPDHRHCBQLPPPCALMWC 472
 DB 383 KYLLKNPKCILDPLLRKDIAAPVCGNEIWEEGECDCGSPADCRN-----PCDDAATC 437
 QY 473 S---GHLNGHAMCQTKHSPWADGTPCGPAQA-CWGGRCI-HMDOLQDFNIPQAGGWGPGW 529
 DB 438 KLPKGAECNGECCDKCKIRKAGTECRPAR-----467
 QY 530 GDC--SRTCGGVQFSSRDCTPVPVRNGGKYCEGRTRFRSCNTEDCPT-----GS 578
 DB 468 DDCDVAEHCTG-----QSAECPRNEFORNGQPC---LNNSGYCVNGDCPIMLNQIALFSP 520
 QY 579 ALTFREEQCAAYNHRITDLF-----KSPFGPMDWVPRYTVGAPQD-QC-KLTQCA 625
 DB 521 SATVAQDSCFQRLNQSYYGYCTKEIYGYKRPF-----CAPODVKCGRLYCLD 569
 QY 626 RAL-----GYVYVLEPR--VVDGTPCSPDSSVCVQGRCI 658
 DB 570 NSPKKNRCKNDYSADENKGIVEPGTKC--EDGKVCINRKCVC 610

Search completed: April 1, 2005, 12:52:34
 Job time : 55 secs

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OM protein - protein search, using sw model

Run on: April 1, 2005, 12:34:02 ; Search time 186 Seconds
(without alignments)
2304.356 Million cell updates/sec

Title: US-09-634-287E-2

Perfect score: 4570

Sequence: 1 MSQTGSHPGIAGRLMGA.....LHRRQAILEILRRPWAQRK 837

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query	Length	DB	ID	Description
1	4570	100.0		837	1	AT54_HUMAN	O75173 homo sapien
2	4563	99.8		837	2	Q6UWA8	Q6UWA8 homo sapien
3	4538	99.3		837	2	Q6P4Q8	Q6P4Q8 homo sapien
4	4200	91.9		839	2	Q7YS95	Q7YS95 bos taurus
5	4106	89.8		845	2	Q8BNJ2	Q8BNJ2 mus musculus
6	4105	89.8		833	2	Q8K384	Q8K384 mus musculus
7	3894	85.2		893	2	Q6A017	Q6A017 mus musculus
8	3218	70.4		630	1	AT54_RAT	Q9esp7 rattus norv
9	2161.5	47.3		967	1	AT51_RAT	Q9wuq1 rattus norv
10	2160.5	47.3		967	2	Q68EJ2	Q68EJ2 rattus norv
11	2158	47.2		968	1	AT51_MOUSE	P97857 mus musculus
12	2135	46.7		967	1	AT51_HUMAN	Q9uh18 homo sapien
13	2127	46.5		967	2	Q8NE26	Q8NE26 homo sapien
14	1998.5	43.7		759	2	Q8HZM8	Q8HZM8 equus cabal
15	1915	41.9		950	1	AT15_HUMAN	Q8te58 homo sapien
16	1842.5	40.3		900	1	AT58_HUMAN	Q9up79 homo sapien
17	1824	39.9		905	1	AT58_MOUSE	P97110 mus musculus
18	1659	36.3		339	2	Q8NEK2	Q8NEK2 homo sapien
19	1576	34.5		930	1	AT55_MOUSE	Q9r001 mus musculus
20	1567.5	34.3		928	2	Q6TV19	Q6TV19 rattus norv
21	1558	34.1		930	1	AT55_HUMAN	Q9una0 homo sapien
22	1547	33.9		1906	1	AT20_MOUSE	P59511 mus musculus
23	1518.5	33.2		867	2	Q66KM3	Q66KM3 xenopus tro
24	1494.5	32.7		1935	1	AT59_HUMAN	Q9p2n4 homo sapien
25	1482	32.4		1911	1	AT20_HUMAN	P59510 homo sapien
26	1386.5	30.3		623	2	Q8BGF4	Q8BGF4 m mus muscu
27	1317	28.8		2165	2	Q19791	Q19791 caenorhabdi
28	1217	26.6		245	1	AT54_BOVIN	Q9tte93 bos taurus
29	1150	25.2		562	1	AT15_MOUSE	P59384 mus musculus
30	1091.5	23.9		1077	1	AT10_HUMAN	Q9h324 homo sapien
31	1087	23.8		192	2	Q95N24	Q95N24 equus cabal

RESULT 1

AT54_HUMAN
ID AT54_HUMAN STANDARD; PRT; 837 AA.
AC Q75173; Q9UN83;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE ADAMTS-4 precursor (EC 3.4.24.82) (A disintegrin and metalloproteinase with thrombospondin motifs 4) (ADAM-TS 4) (ADAM-TS4) (Aggrecanase 1) (ADMP-1).
DE Name=ADAMTS4; Synonyms=KIAA0688;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98403880; PubMed=9734811;
RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RA "Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
RL DNA Res. 5:169-176(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99286303; PubMed=10356395; DOI=10.1126/science.284.5420.1664;
RA Tortorella M.D., Burn T.C., Pratta M.A., Abbaszade I., Hollis J.M., Liu R.-Q., Rosenfeld S.A., Copeland R.A., Decicco C.P., Wynn R., Rockwell A., Yang F., Duke J.L., Solomon K., George H., Bruckner R., Nagase H., Itoh Y., Ellis D.M., Ross H., Wiswall B.H., Murphy K., Hillman M.C. Jr., Hollis G.P., Newton R.C., Magolda R.L., Trzaskos J.M., Arner E.C.;
RA "Purification and cloning of aggrecanase-1: a member of the ADAMTS family of proteases.";
RL Science 284:1664-1666(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Sawaji Y., Nagase H., Saklatvala J., Clark A.R.;
RT "ADAMTS-4 genomic locus.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP PARTIAL SEQUENCE, AND CHARACTERIZATION.
RX MEDLINE=20400518; PubMed=10827174; DOI=10.1074/jbc.M001065200;
RA Tortorella M.D., Pratta M.A., Liu R.-Q., Abbaszade I., Ross H., Burn T.C., Arner E.C.;
RT "The thrombospondin motif of aggrecanase-1 (ADAMTS-4) is critical for aggrecan substrate recognition and cleavage.";
RL J. Biol. Chem. 275:25791-25797(2000).
CC -!- FUNCTION: Cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. May play an important role in the destruction of aggrecan in arthritic diseases. Could also be a critical factor in the exacerbation of neurodegeneration in

Q8ch80 cavia porce
Q8cg28 mus musculus
Q68a9 mus musculus
Q9ukp4 homo sapien
Q6p7j9 homo sapien
Q7ksh7 drosophila
P58397 homo sapien
Q8sxb0 drosophila
Q6p4r5 homo sapien
Q9w493 drosophila
Q6v228 mus musculus
Q8te60 homo sapien
Q9ukp5 homo sapien
Q8k206 mus musculus

ALIGNMENTS


```
Db 359 ANHELGHVFMHNDNSKQCTGLNGPESTSRHVNAPVMAHVDPEEPSPCSARFITDFLDN 418
QY 419 GYGHCLLDKPEALPHLPVTFPGKDYADROCOQTFFGDSRHCQLPPLPPCAALWCSGHLNG 478
Db 419 GFHCLLDKPEALPHLPVTFPGKDYADROCOQTFFGDSRHCQLPPLPPCAALWCSGHLNG 478
QY 479 HAMCQTKHSPWADGTPCGPAQACMGGRCLHMDQLQDFNIPQAGGWGPGWGDSCRTCGG 538
Db 479 HAMCQTKHSPWADGTPCGPAQACMGGRCLHMDQLQDFNIPQAGGWGPGWGDSCRTCGG 538
QY 539 GVQFSSRDCTPRVPRNGKXCEGRTRFRSCNTEDCTGSAITFRBEOCAAYNHRDLPK 598
Db 539 GVQFSSRDCTPRVPRNGKXCEGRTRFRSCNTQDCPTGSAITFRBEOCAAYNHRDLPK 598
QY 599 SPFGPMWVPRYTGVAPODCKLTQARALGYVYVLEPRVVDGTPCSPDSSSSVCVQGRCI 658
Db 599 NFGPMWVPRYTGVAPODCKLTQTRALGYVYVLDPRVADGTPCSPDSSSSVCVQGRCI 658
QY 659 HAGCDRIIGSKKFKDKCMVCGDGGSCGSKGSGFRKFRYGNNVVTIPAGATHILVRQOG 718
Db 659 HAGCDRIIGSKKFKDKCMVCGDGGSCGSKGSGFRKFRYGNNVVTIPAGATHILVRQOG 718
QY 719 NPGHRIYLAALKLPDGSYALNGEYTLMPSTDVLPQAVSLRYSGATASETLSGHGPLA 778
Db 719 SPSVRSLYLALKLPDGSYALNGEYTLIPSTDVLPQAVSLRYSGATASETLSGHGPLA 778
QY 779 QPULTQVLVAGNPQDRLRYSFFV--PRPTPTPTPTQDMLHRRRAQILEILRRRWAGR 836
Db 779 EPILTQVLVAGNPQDRLRYSFFVPRPVPSTPTPTQDMLHRRRAQILEILRRRWAGR 838
QY 837 K 837
Db 839 K 839

RESULT 5
Q8BNJ2 PRELIMINARY; PRT; 845 AA.
AC Q8BNJ2;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Mus musculus 9 days embryo whole body cDNA, RIKEN full-length enriched
DE library, clone:D030041M02 product:a disintegrin-like and
DE metalloprotease (repolysin type) with thrombospondin type 1 motif, 4,
DE full insert sequence.
GN Name=Adams4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA The PANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
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RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX STRAIN=C57BL/6J; Arakawa T., Bono H., Carninci P.,
RA Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
RA Fukuda S., Furuno M., Hanagaki T., Hiraoka T., Hirozane T.,
RA Hayashida K., Hayatsu N., Hiramoto K., Kagawa I., Kasukawa T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Konno H., Kouda M., Koya S.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh K., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toy T., Yasunishi I., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK083534; BAC38944.1; -.
DR HSSP; P07996; ILSL.
DR MEROPS; M12.221; -.
DR MGD; MGI:1339949; Adams4.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP 1.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR PRINTS; PR01705; TSP1; 1.
DR SMART; SM00209; TSP1; 1.
DR PROSITE; PS00215; ADAM_MEPRO; 1.
DR PROSITE; PS00092; TSP1; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Integrin; Metalloprotease; Protease.
SQ SEQUENCE 845 AA; 91238 MW; B496C3190D1A9225 CRC64;
Query Match 89.8%; Score 4106; DB 2; Length 845;
Best Local Similarity 90.5%; Pred. No. 3.8e-256;
Matches 758; Conservative 22; Mismatches 52; Indels 6; Gaps 2;
QY 1 MSQTGSHPGRGLAGRWLWGAQPCLLPIVPLSWLVLMLLLLLASLPASLPREEE 60
Db 13 MSQMGHPRRLTGHMLQRFQPCJ-----PLHTVQVRRLLLAFLSLAWPASPREEE 67
QY 61 IVPPEKING-SVLPFGSGAPARLLCRQAGETLLEQLLEQDSGVQVREGTLVYLGQAPELL 119
Db 68 IVPPEKINGSSILPGSGVPARLLYRLPARGEMLLLEQDPGVQVREGTLVYLGQAPELL 127
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QY	120	GGAEPTGTYLTGTINGDPESVASLHWDGALLGVLYQVRAELHLQPLEGGTPNSAGGPGAH	179
Db	128	GGAEPTGTYLTGTINGDPESVASLHWDGALLGVLYQVRAELHLQPLEGGTPNSAGGPGAH	187
QY	180	ILRRKSPASQGGPNCVAKPLGSPSPRRPRRAKRFASLSRFVETLVVADDDKMAAFHAGLGLK	239
Db	188	ILRRKSPASQGGPNCVAKPLGSPSPRRPRRAKRFASLSRFVETLVVADDDKMAAFHAGLGLK	247
QY	240	RYLLTVMAAAAKAFKHPISIRNPVSLVTRVLVILGSGEGPQVGPSPAAQTLRFCAWQRL	299
Db	248	RYLLTVMAAAAKAFKHPISIRNPVSLVTRVLVILGSGEGPQVGPSPAAQTLRFCAWQRL	307
QY	300	NTPEDSDPHFDFTAILFTRODLGCVSTCDTLGMADVGTVCDPARSCAIVDDGLQSAFTA	359
Db	308	NTPEDSDPHFDFTAILFTRODLGCVSTCDTLGMADVGTVCDPARSCAIVDDGLQSAFTA	367
QY	360	AHELGHVFNMLHDSKPCISLNGPLSTSRHVMAFVMAHVDPPEPWPSPCSARFITDFLDNG	419
Db	368	AHELGHVFNMLHDSKPCISLNGPLSTSRHVMAFVMAHVDPPEPWPSPCSARFITDFLDNG	427
QY	420	YGHCLLDKPEAPLHLPVTFPGKYDADROCOLTFGPDSPHRCPOLPPPCAAALWCSGHLNGH	479
Db	428	YGHCLLDKPEAPLHLPVTFPGKYDADROCOLTFGPDSPHRCPOLPPPCAAALWCSGHLNGH	487
QY	480	AMCOTKHPWADGTFPGCPAQACMGRCCLHMDQLODFNIPOAGGWPWGPWDCSRTCGGG	539
Db	488	AMCOTKHPWADGTFPGCPAQACMGRCCLHMDQLODFNIPOAGGWPWGPWDCSRTCGGG	547
QY	540	VQFSRDCTRPVPRNGKCYCEGRTRFRSNTEDCPTGSAITFREOCAYNHTDLFKS	599
Db	548	VQFSRDCTRPVPRNGKCYCEGRTRFRSNTEDCPTGSAITFREOCAYNHTDLFKS	607
QY	600	PPGMDWVPRYTGVAPODOCKLTQARALGYVYVLEPRVVDGTPCSPDSSVVCQGRCH	659
Db	608	PPGMDWVPRYTGVAPODOCKLTQARALGYVYVLEPRVVDGTPCSPDSSVVCQGRCH	667
QY	660	AGCDRIIGSKKKFKCMVCGGSGCSKQSGSKFRFYGNVVTIIPAGTHILVRQGN	719
Db	668	AGCDRIIGSKKKFKCMVCGGSGCSKQSGSKFRFYGNVVTIIPAGTHILVRQGN	727
QY	720	PCHRSYIALKLPGSYALNBEYTLMPSPDTDWLPVAVLSYSGATASETLSHGFLAQ	779
Db	728	SGLSKSYIALKLPGSYALNBEYTLMPSPDTDWLPVAVLSYSGATASETLSHGFLAQ	787
QY	780	PLTLQVLVAGNPQDTRLSYFVPRPTSTPRPTQDWLHRAQLLEILRRPWRGRK	837
Db	788	PLTLQVLVAGNPQDTRLSYFVPRPTSTPRPTQDWLHRAQLLEILRRPWRGRK	845
RESULT 6			
Q8K384			
ID	Q8K384	PRELIMINARY; PRT; 833 AA.	
AC	Q8K384;		
DT	01-OCT-2002 (TrEMBLrel. 22, Created)		
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Adams4 protein.		
GN	Name=Adams4;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RC	SEQUENCE FROM N.A.		
RC	STRAIN=FVB/N; TISSUE=Mammary tumor. C3;		
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,		
RA	Fahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=FVB/N; TISSUE=Mammary tumor. C3;		
RA	Strausberg R.;		
RL	Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC027773; AAH27773.1; -.		
DR	HSSP; P07996; 1LSL.		
DR	MEROPS; M12.221; -.		
DR	MGI; M1339949; Adams4.		
DR	GO; GO:0004222; F:metalloendopeptidase activity; IEA.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPR010294; ADAM spacer1.		
DR	InterPro; IPR001590; Peptidase M12B.		
DR	InterPro; IPR006025; Pept. M_Zn_BS.		
DR	InterPro; IPR000884; TSP1_		
DR	InterPro; IPR000885; TSP1.		
DR	Pfam; PF05986; ADAM spacer1; 1.		
DR	Pfam; PF01421; Reprolysin; 1.		
DR	Pfam; PF00090; TSP 1; 1.		
DR	PRINTS; PR01705; TSP1REPEAT.		
DR	SMART; SM00209; TSP1_1.		
DR	PROSITE; PS0215; ADAM MEPRO; 1.		
DR	PROSITE; PS0092; TSP1; 1.		
DR	PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.		
SQ	SEQUENCE 833 AA; 90097 MW; 4CEC83DFBC3AA619 CRC64;		
Query Match 89.8%; Score 4105; DB 2; Length 833;			
Best Local Similarity 90.5%; Pred. No. 4.4e-256;			
Matches 758; Conservative 22; Mismatches 52; Indels 6; Gaps 2;			
QY	1	MSQTGSHPCRGGLAGRWLGAQPCILLPIVPLSWLWLLILLASLPSARLASPLREE	60
Db	1	MSQWGLHPRRLTGHWRFPCL-----PLHTVQWRLLLLAFLLSLWAPSLREE	55
QY	61	IVFPEKING-SVLPGSGAPARLLCRLOAFGETLLLEQDSGVQVVEGLTVYLQAPELL	119
Db	56	IVFPEKINGSSILPGSGVPARLLYRLPAFGEMLLLEQDPGVQVVEGLTVYLQAPML	115
QY	120	GGABPGTYLTGTINGDPESVASLHWDGALLGVLYQVRAELHLQPLEGGTPNSAGGPGAH	179
Db	116	GGABPGTYLTGTINGDPESVASLHWDGALLGVLYQVRAELHLQPLEGGTPNSAGGPGAH	175
QY	180	ILRRKSPASQGGPNCVAKPLGSPSPRRPRRAKRFASLSRFVETLVVADDDKMAAFHAGLGLK	239
Db	176	ILRRKSPASQGGPNCVAKPLGSPSPRRPRRAKRFASLSRFVETLVVADDDKMAAFHAGLGLK	235
QY	240	RYLLTVMAAAAKAFKHPISIRNPVSLVTRVLVILGSGEGPQVGPSPAAQTLRFCAWQRL	299
Db	236	RYLLTVMAAAAKAFKHPISIRNPVSLVTRVLVILGSGEGPQVGPSPAAQTLRFCAWQRL	295
QY	300	NTPEDSDPHFDFTAILFTRODLGCVSTCDTLGMADVGTVCDPARSCAIVDDGLQSAFTA	359
Db	296	NTPEDSDPHFDFTAILFTRODLGCVSTCDTLGMADVGTVCDPARSCAIVDDGLQSAFTA	355
QY	360	AHELGHVFNMLHDSKPCISLNGPLSTSRHVMAFVMAHVDPPEPWPSPCSARFITDFLDNG	419
Db	356	AHELGHVFNMLHDSKPCISLNGPLSTSRHVMAFVMAHVDPPEPWPSPCSARFITDFLDNG	415
QY	420	YGHCLLDKPEAPLHLPVTFPGKYDADROCOLTFGPDSPHRCPOLPPPCAAALWCSGHLNGH	479

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Db 416 YGCHLLDKPEAPLHLPATPGKYDADROCLTFGPDSSHCPLQPPPCAAALMCSGHLNGH 475
QY 480 AMQOTKHSWADTTCGPAQACMGGRCLHMDQLQDENIPQAGGWPWGWDGDCSRTCCGG 539
Db 476 AMQOTKHSWADTTCGSSQACMGGRCLHVDKDFNVPQAGGWPWGWDGDCSRTCCGG 535
QY 540 VPFSSRDCTRPVPRNGGKCEGRTFRSCNTDCTGTSALTFRBQCAAYNHRITLFXS 599
Db 536 VQFSSRDCTRPVPRNGGKCEGRTFRSCNTDCTGTSALTFRBQCAAYNHRITLFXS 595
QY 600 FPGMDWPRYTCVAPQDOCKLTCQARALGYVYVLEPRVVDGTPCSPDSSVVCQGRCH 659
Db 596 FPGMDWPRYTCVAPQDOCKLTCQARALGYVYVLEPRVVDGTPCSPDSSVVCQGRCH 655
QY 660 AGCDRIIGSKKPKDKMVCGGSGCSKQSGSRKRYGYNVVVTIPAGATHILVRQGN 719
Db 656 AGCDRIIGSKKPKDKMVCGGSGCSKQSGSRKRYGYSVDVVTIPAGATHILVRQGN 715
QY 720 PGRHSYIALKLPDGSYALNGEYTLMPSTDVVLPQAVSLRYSGATAASETLSGHGFLAQ 779
Db 716 SGLKSIYALKLPDGSYALNGEYTLMPSTDVVLPQAVSLRYSGATAASETLSGHGFLAQ 775
QY 780 PLTLQVLVAGNPQDTRLSFFVPRTPSTPRTPQDHLHRAQIIEILRRRPWGRK 837
Db 776 PLTLQVLVAGNPQARLRSFFVPRVPTPRPPQDQLQRAEILKILKRPWGRK 833

RESULT 7
Q6A017 PRELIMINARY; PRT; 893 AA.
ID AC Q6A017;
DC 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MKIA0688 protein (Fragment).
GN Name=mkIAA0688;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]_Sequence from N.A.
RP TISSUE=Brain;
RC Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,
RA Nagase T., Ohara O., Koga H.;
RT "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:
RT cDNAs Identified by Screening of Terminal Sequences of cDNA Clones
RT Randomly Sampled from Size-Fractionated Libraries.";
RL DNA Ref. 11:205-218(2004).
DR EMBL; AK173001; BAD32279.1; -.
DR GO; GO:004222; F:metallopeptidase activity; IEA.
DR GO; GO:000508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006586; ADAM cysteine.
DR InterPro; IPR010294; ADAM spacer1.
DR InterPro; IPR001590; Peptidase M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR000885; TSP_1.
DR Pfam; PF05986; ADAM spacer1; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR Pfam; PF00090; TSP_1; 1.
DR PRINTS; PR01705; TSP1RHEPAT.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00209; TSP1; 1.
DR PROSITE; PS0215; ADAM MEPRO; 1.
DR PROSITE; PS0092; TSP1; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 893 AA; 96389 MW; F4F12254E2CCF8F CRC64;
```

```
Query Match 85.2%; Score 3894; DB 2; Length 893;
Best Local Similarity 86.8%; Pred. No. 1.9e-242;
Matches 732; Conservative 25; Mismatches 68; Indels 18; Gaps 5;

QY 1 MSQTGSHPGRLAGRWGAQPCLLPIVPLSLVWMLLLLLLASLLPSARLASPLPREE 60
Db 63 MSQMGHLHPRGLTGHWRFPQCL-----PLHTVQWRRLLLLLLAFLSLAWPASPLPREE 117
QY 61 IVFPEKLNG-SVLPGSGAPARLLCRLOAFGETLLLELEODSGVQVEGLTVQYLGQAPELL 119
Db 118 IVFPEKLNGSSILPGSGVPARLLYRLPAFGEMLLLEQDPGVQVEGLTVQYLGQAPELL 177
QY 120 GGAEPCTYLTGTINGDPESVASLHMDGGALLGLVQYRGAEHLHLPLEGGTPNSAGGFGAH 179
Db 178 GGAEPCTYLTGTINGDPESVASLHMDGGALLGLVQYRGAEHLHLPLEGGALNSAGGFGAH 237
QY 180 ILRRKSPASQGMCMNVKAPLSPSPRPRARAKRFASLSRFVETLVVADDKMAAFHAGLXK 239
Db 238 ILRRKSPASQGMCMNVKAPLSPSPSRRTKRFASLSRFVETLVVADDKMAAFHAGTGLK 297
QY 240 RYLLTVMAAAAKAFKHPISIRNPVSLVTVTRLVILGSGEGPOVG-----PSAAQTLSRFCA 294
Db 298 RYLLTVMAAAAKAFKHPISIRNPVSLVTVTRLVILGSGEGPOVG-----PSAAQTLSRFCA 353
QY 295 WORGMLTPEDSDPDHEDTALIFETRODLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQ 354
Db 354 ---GASTPLTTQLITLTTALIFETRODLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQ 410
QY 355 SAFTAAHELGHVFNMLHDNSKPCISLNGPLSTSRHVMAVMAHVDPEEPWSPCSARPTD 414
Db 411 SAFTAAHELGHVFNMLHDNSKPCITNLNGQSSSRHVMAVMAHVDPEEPWSPCSARPTD 470
QY 415 FLNDNGYGHCLLDKPEAPLHLPVTFPGKYDADROCLTFGPDSSHCPLQPPPCAAALMCSG 474
Db 471 FLNDNGYGHCLLDKPEAPLHLPVTFPGKYDADROCLTFGPDSSHCPLQPPPCAAALMCSG 530
QY 475 HLNHAMCOTKHSWADTTCGPAQACMGGRCLHMDQLQDENIPQAGGWPWGWDGDCSR 534
Db 531 HLNHAMCOTKHSWADTTCGSSQACMGGRCLHVDKDFNVPQAGGWPWGWDGDCSR 590
QY 535 TCGGVQVFSRDCTRPVPRNGGKCEGRTFRSCNTDCTGTSALTFRBQCAAYNHRIT 594
Db 591 TCGGVQVFSRDCTRPVPRNGGKCEGRTFRSCNTDCTGTSALTFRBQCAAYNHRIT 650
QY 595 DLFKSPFGPMDMVPRYTVGAPQDOCKLTCQARALGYVYVLEPRVVDGTPCSPDSSVVCVQ 654
Db 651 DLFKSPFGPMDMVPRYTVGAPQDOCKLTCQARALGYVYVLEPRVVDGTPCSPDSSVVCVQ 710
QY 655 GRCIHAGCDRIIGSKKPKDKMVCGGSGCSKQSGSRKRYGYNVVVTIPAGATHILV 714
Db 711 GRCIHAGCDRIIGSKKPKDKMVCGGSGCSKQSGSRKRYGYSVDVVTIPAGATHILV 770
QY 715 ROQGNPHRHSIYALKLPDGSYALNGEYTLMPSTDVVLPQAVSLRYSGATAASETLSGH 774
Db 771 ROQGNPHRHSIYALKLPDGSYALNGEYTLMPSTDVVLPQAVSLRYSGATAASETLSGH 830
QY 775 GPLAQLTLQVLVAGNPQDTRLSFFVPRTPSTPRTPQDHLHRAQIIEILRRRPWA 834
Db 831 GPLAQLTLQVLVAGNPQARLRSFFVPRVPTPRPPQDQLQRAEILKILKRPWMA 890
QY 835 GRK 837
Db 891 GRK 893

RESULT 8.
ATSA RAT
ID ATSA RAT
AC Q9ESP7; Q9ESP6; Q9ESP8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE ADAMTS-4 precursor (BC 3.4.24.82) (A disintegrin and metalloproteinase
```

with thrombospondin motifs 4) (ADAM-TS 4) (ADAM-TS4) (Aggrecanase 1)
(Fragment).
GN Names=Adamts4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Brain;
RX MEDLINE=20415831; PubMed=10361558; DOI=10.1016/S0304-3940(00)01285-4;
RA Satoh K., Suzuki N., Yokota H.;
RT "ADAMTS-4 (a disintegrin and metalloproteinase with thrombospondin
RT motifs) is transcriptionally induced in beta-amyloid treated rat
RT astrocytes.";
RL Neurosci. Lett. 289:177-180(2000).
CC -1- FUNCTION: Cleaves aggrecan, a cartilage proteoglycan, and may be
CC involved in its turnover. May play an important role in the
CC destruction of aggrecan in arthritic diseases. Cleaves aggrecan at
CC the 392-Glu-[Ala-393 site.
CC -1- CATALYTIC ACTIVITY: Glutamyl endopeptidase; bonds cleaved include
CC 370-Thr-Glu-Glu-[Ala-Arg-Gly-Ser-377 in the interglobular
CC domain of mammalian aggrecan.
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
CC matrix (By similarity).
CC -1- TISSUE SPECIFICITY: Brain specific.
CC -1- DOMAIN: The spacer domain and the TSP type-1 domains are important
CC for a tight interaction with the extracellular matrix.
CC -1- PM: The precursor is cleaved by a furin endopeptidase.
CC -1- SIMILARITY: Belongs to the peptidase M12B family.
CC -1- SIMILARITY: Contains 1 disintegrin-like domain.
CC -1- SIMILARITY: Contains 1 TSP type-1 domain.
CC
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CC
CC EMBL; AB042272; BAB16474.1; --
CC EMBL; AB042271; BAB16473.1; --
CC EMBL; AB042273; BAB16475.1; --
CC HSSP; P07996; 1LSL.
CC MEROPS; M12.221; --
CC RGD; 621242; Adamts4.
CC InterPro; IPR010294; ADAM spacer1.
CC InterPro; PS001762; Disintegrin.
CC InterPro; IPR006025; Pept_M_Zn_BS.
CC InterPro; IPR001590; Peptidase_M12B.
CC InterPro; IPR000884; TSP1.
CC InterPro; IPR008085; TSP 1.
CC Pfam; PF05986; ADAM spacer1; 1.
CC Pfam; PF01421; Reprlysine; 1.
CC Pfam; PF00090; TSP_1; 1.
CC PRINTS; PR01705; TSP1REPEAT.
CC SMART; SM00209; TSP1; 1.
CC PROSITE; PS00215; ADAM_MEPPO; 1.
CC PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
CC PROSITE; PS00214; DISINTEGRIN_2; FALSE_NEG.
CC PROSITE; PS00092; TSP1; 1.
CC PROSITE; PS00142; ZINC_PROTEASE; 1.
CC PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Extracellular matrix; Glycoprotein; Hydrolase; Metalloprotease; Zinc;
KW Zymogen.
FT NON TER 1 1
FT PROPEP <1 5 By similarity.
FT CHAIN 6 630 ADAMTS-4.
FT DOMAIN 6 232 Metalloprotease.
FT DOMAIN 233 303 Disintegrin-like.
FT DOMAIN 313 368 TSP type-1.
FT DOMAIN 368 478 Cys-rich.

FT	DOMAIN	479	630	Spacer.
FT	DOMAIN	40	45	Poly-Ala.
FT	METAL	154	154	Zinc (catalytic) (By similarity).
FT	ACT SITE	155	155	By similarity.
FT	METAL	158	158	Zinc (catalytic) (By similarity).
FT	METAL	164	164	Zinc (catalytic) (By similarity).
FT	CARBOHYD	96	96	N-linked (GlcNAc...) (Potential).
FT	CARBOHYD	474	474	N-linked (GlcNAc...) (Potential).
FT	CARBOHYD	630	630	AA; 68384 MW; 63A428753167C7EF CRC64;
FT	SEQ			
Query Match				
Best Local Similarity 70.4%; Score 3218; DB 1; Length 630;				
Matches 581; Conservative 20; Mismatches 29; Indels 0; Gaps 0;				
QY	208	RRARFASLSRFVETLVVADDKMAAFHAGLKYRLTYLWMAAAKAFKHPHSIRNPVSVLT	267	
DB	1	RRTRFASLSRFVETLVVADDKMAAFHAGLKYRLTYLWMAAAKAFKHPHSIRNPVSVLT	60	
QY	268	RLVILSGEGEPQVGPSSAAQTLRSFCAMQRLNPEDSDPHFTAILFTRODLCGVSTC	327	
DB	61	RLVILSGEGEPQVGPSSAAQTLRSFCAMQRLNPEDSDPHFTAILFTRODLCGVSTC	120	
QY	328	DTLGMADVGTCDPARSCAIVDDGLOSAFTAHELGHVFNMLHNSKPCISLNGPLSTS	387	
DB	121	DALGMAGVGTCDPARSCAIVDDGLOSAFTAHELGHVFNMLHNSKPCANLNGQSSS	180	
QY	398	RHVMAPVMAHVDPEPNSPCSAFTITDLDNGYGHCLLDKPEAPLHLPVTPGKDYDADR	447	
DB	181	RHVMAPVMAHVDPEPNSPCSAFTITDLDNGYGHCLLDKPEAPLHLPVTPGKDYDADR	240	
QY	448	QCQLTFGPDSSRHCPOLPFPCCALWCASHLNGHAMQTKHSPWADGTCGPAQACMGGRCL	507	
DB	241	QCQLTFGPDSSRHCPOLPFPCCALWCASHLNGHAMQTKHSPWADGTCGPAQACMGGRCL	300	
QY	508	HNDQLQDNIPACAGMGWPGMDCSRTCSCGGVQFSSRDCTPVPVPRNGGKYCEGRTRPFR	567	
DB	301	HVDQLQDNIPACAGMGWPGMDCSRTCSCGGVQFSSRDCTPVPVPRNGGKYCEGRTRPFR	360	
QY	568	SCNTEDECPTGSALTTFREOCAYNHRDILFKSPGPMQVRYTGVAPQDCKLTCQARA	627	
DB	361	SCNTRKNCPHSALTTFREOCAYNHRDILFKSPGPMQVRYTGVAPQDCKLTCQARA	420	
QY	628	LGYYVLEPRVVDGTPCSPDSSVQVQRCIHAGCDRIIGSKKFKDKMVCQGGDGGCSK	687	
DB	421	LGYYVLEPRVVDGTPCSPDSSVQVQRCIHAGCDRIIGSKKFKDKMVCQGGDGGCSK	480	
QY	688	QSGSFRKFRYGYNNVVTIPAGATHILVROQGNPHRSIYLAKLPDGSYALNGEYTLMS	747	
DB	481	QSGSFRKFRYGYNNVVTIPAGATHILVROQGNPHRSIYLAKLPDGSYALNGEYTLMS	540	
QY	748	PTDVLPGAVSLRYSGATASETLSGHGPIAQLTLQVLVAGNPQDTRLYRFFVPRPTP	807	
DB	541	STDVLPVAVSLRYSGATASETLSGHGPIAQLTLQVLVAGNPQDTRLYRFFVPRPTP	600	
QY	808	STPRPTQDVLHRRAOILEILRRRPPWAGRK	837	
DB	601	STPRPTQDVLHRRAOILEILRRRPPWAGRK	630	
RESULT 9				
ATSI	RAT			
ID	ATSI	RAT	STANDARD;	PRT; 967 AA.
AC	Q9WUQ1; Q9ER11;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	ADAMTS-1 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 1) (ADAM-TS 1) (ADAM-TS1).			
GN	Name=Adamts1.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			

[1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RA Liu X., Tu Y., Yin T., Johnstone E.M., Stephenson D.T., Clemens J.A.,
 RA Little S.P.;
 RT Induction of a disintegrin and metalloprotease with the
 RT thrombospondin type I motif (ADAMTS).";
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE OF 18-967 FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=20304099; PubMed=10847486;
 RA Diamantis I., Luehli M., Hoesli M., Reichen J.;
 RT "Cloning of the rat ADAMTS-1 gene and its down regulation in
 RT endothelial cells in cirrhotic rats.";
 RL Liver 20:165-172(2000).
 CC -1- FUNCTION: Cleaves aggrecan, a cartilage proteoglycan, and may be
 CC involved in its turnover. Has angiogenic inhibitor activity (By
 CC similarity). Active metalloprotease, which may be associated with
 CC various inflammatory processes as well as development of cancer
 CC cachexia. May play a critical role in follicular rupture (By
 CC similarity).
 CC -1- CATALYTIC ACTIVITY: Cleaves aggrecan at the 1683-Glu-Leu-1684
 CC site, within the chondroitin sulfate attachment domain.
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
 CC matrix (By similarity).
 CC -1- INDUCTION: Down-regulated in endothelial cells derived from
 CC cirrhotic liver.
 CC -1- DOMAIN: The spacer domain and the TSP type-1 domains are important
 CC for a tight interaction with the extracellular matrix.
 CC -1- PTM: The precursor is cleaved by a furin endopeptidase (By
 CC similarity).
 CC -1- SIMILARITY: Belongs to the peptidase M12B family.
 CC -1- SIMILARITY: Contains 1 disintegrin-like domain.
 CC -1- SIMILARITY: Contains 3 TSP type-1 domains.
 CC -----
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 CC -----
 DR EMBL: AF149118; AAD34012.1; -;
 DR EMBL: AF304446; AG29823.1; -;
 DR HSSP: P07996; ILSL.
 DR MEROPS: M12.222; -;
 DR InterPro: IPR006586; ADAM_cysteine.
 DR InterPro: IPR010294; ADAM_spacer1.
 DR InterPro: IPR001762; Disintegrin.
 DR InterPro: IPR006025; Pept_M_Zn_BS.
 DR InterPro: IPR001590; Peptidase_M12B.
 DR InterPro: IPR002870; Peptidase_M12B_N.
 DR InterPro: IPR000884; TSP1.
 DR InterPro: IPR008085; TSP1.
 DR Pfam: PF05986; ADAM_spacer1.1.
 DR Pfam: PF01421; Reprolysin; 1.
 DR Pfam: PF01562; Pep_M12B_propep; 1.
 DR Pfam: PF00090; TSP_1; 3.
 DR PRINTS: PR01705; TSP1REPEAT.
 DR SMART: SM00608; ACR; 1.
 DR SMART: SM00209; TSP1; 3.
 DR PROSITE: PS00215; ADAM_MEROP; 1.
 DR PROSITE: PS00427; DISINTEGRIN_1; FALSE_NEG.
 DR PROSITE: PS00214; DISINTEGRIN_2; FALSE_NEG.
 DR PROSITE: PS00092; TSP1; 3.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 KW Extracellular matrix; Glycoprotein; Heparin-binding; Hydrolase;
 KW Metalloprotease; Repeat; Signal; Zinc; Zymogen.
 FT SIGNAL 1 54 Potential.
 FT PROPEP 55 252 By similarity.

FT	CHAIN	253	967	ADAMTS-1.
FT	DOMAIN	253	475	Metalloprotease.
FT	DOMAIN	476	558	Disintegrin-like.
FT	DOMAIN	559	614	TSP type-1 1.
FT	DOMAIN	616	724	Cys-rich.
FT	DOMAIN	725	857	Spacer.
FT	DOMAIN	854	910	TSP type-1 2.
FT	DOMAIN	911	967	TSP type-1 3.
FT	DOMAIN	194	198	Poly-Arg.
FT	SITE	205	205	Cysteine switch (Potential).
FT	METAL	401	401	Zinc (catalytic) (By similarity).
FT	ACT_SITE	402	402	By similarity.
FT	METAL	405	405	Zinc (catalytic) (By similarity).
FT	METAL	411	411	Zinc (catalytic) (By similarity).
FT	CARBOHYD	547	547	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	720	720	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	764	764	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	782	782	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	945	945	N-linked (GlcNAc. .) (Potential).
FT	CONFLICT	21	21	I -> V (in Ref. 2).
FT	CONFLICT	26	31	KFRSSQ -> RSRGSL (in Ref. 2).
FT	CONFLICT	49	49	V -> A (in Ref. 2).
FT	CONFLICT	72	72	R -> P (in Ref. 2).
FT	CONFLICT	79	79	L -> TR (in Ref. 2).
FT	CONFLICT	249	249	R -> G (in Ref. 2).
FT	CONFLICT	262	265	TMLV -> NLKK (in Ref. 2).
FT	CONFLICT	607	607	S -> F (in Ref. 2).
FT	CONFLICT	936	936	L -> V (in Ref. 2).
FT	CONFLICT	962	962	I -> T (in Ref. 2).
SQ	SEQUENCE	967 AA;	105705 MW;	F93C864F6DCDB4CF CRC64;

QY	37	LLLLLLAS--LPSARIA--SPLPREEEIVFPKINGSVLPVPGSGAPARLLCRLOAFQETL	92
Db	35	MLLLLLASITMLLCVRGAHGRPTDEELVLP-----SLERARGHDSHTLLRLDAFQQL	89
QY	93	LLELEODSGVQVGLTVQVLOQAPELLGGAEE-----PGTYLTGTNGDPESVASL	142
Db	90	HLKLPDPSGFLAPGFTLTQTVGRSP-----GSEAHLDPDGLAHCFYSGTVNGDSSAAAL	145
QY	143	HWDGGALLGVLRGAELHLQP-----LEGGTP--NSAGGPGAHILRRKSPASQGP	192
Db	146	SLCEG--VRGAFYLGEEFFIQAPAVATERLVAEPKEESIAPRFHLARRRGSG--GA	203
QY	193	MCNV-----KAPLGSPSP-----RPR-----RAKRFASLSRFVETL	223
Db	204	KCGVMDDEETLPTNSGREGSONTPDQWPLRNPTQAGAKPTGPGSIRKKRFVSPRYVETM	263
QY	224	VVADDKMAAPHGAGLAKRYLLTWMAAAAKAFKPSIRNPVSLVTRVLVLGSGEGGPOVGP	283
Db	264	LVAQSMADFHGSLGKHYLLTLFSAARFYKHSIRNSISLVVVKILVIYEEQKPEVTS	323
QY	284	SAATLRSCAWQGLNTPEDSDPHDFTAILTRQDLCGVSTCDTLGMADVGTVCDFPAR	343
Db	324	NAALTNRFCQKQHSNPSDRDPEHYDTAILTRQDLCGSHCTDLGMADVGTVCDFPSR	383
QY	344	SCAIVEDDGLQSAFTAAHGLGHVFNHMLHNSKPCISLNGPLSTSRHVMAPVMAHVDPEEP	403
Db	384	SCSVIEDDGLQAAFTTAHELGHVFNHMPHDDAKHCASFNG--VSGDSHLMASMLSLDSHQP	442
QY	404	WSPCSARFITDFLDNGVGHCLLDKPEAPLHLPVTFPGKYDADRQCCLTGPDSRHCPQL	463
Db	443	WSPCSAYMVTSLFDNGHGBCLMDKPNPIKLPDLPGLTYDANRQCQFTTGEESTHCPDA	502
QY	464	PPPCAALWCSGHLNGHAMCOTKHSPPWADGTPCPCPAQACMGCRCLHMDQLQDFNIPAGGW	523
Db	503	ASTCSTLWCTGTSGGLLVCTQKHFPWADGTSCEGKWCVSCKVNTDKMFKFATPVHGSW	562
QY	524	GPWGPNGDCSRTCGGVQVFSRDCRTPVPVPRNGKYCEGRTRFRSCNTEDCPTGSAITFR	583

Query Match 47.3%; Score 2161.5; DB 1; Length 967;
 Best Local Similarity 49.5%; Pred. No. 9.8e-131;
 Matches 415; Conservative 137; Mismatches 217; Indels 69; Gaps 16;

Db 563 GPWPGWDCSRTCGGQVQYTMRECDNPVKNGKYCEGKRVYRSCNIEDCPDNNKTFR 622
QY 584 EQCAAYNHRHTLDFKSPGPMWDRYRTGVAPODQCKLTQARALGYVYVLEPRVVDGTP 643
Db 623 EEQCEAHNEFSKASFGNEPTVETWTPKYAGVSPKDRCKLTCEAKGIGYFVLQPKVVDGTP 682
QY 644 CSPDSSVVCQRCIHAGCDRIIGSKKFKDKCMVCGDGGSGSKSGSPFRKFRYGNVNV 703
Db 683 CSPDSTSVCCVQGVKAGCDRIIDSKKFKDKCGVCGGSGSTCKLSGTVSTRPGVHDIV 742
QY 704 TIPAGATHILVROQGNPHRS--IYLALKLPDGSYALNGEYTIMSPDTPVLPGAVSLRY 761
Db 743 TIPAGATNIEVKHNRPNRSGNNGSFLAIRAADGTYLNGNFTLSTLEQDLTYKGTV-LRY 801
QY 762 SGATASETLSGHGFLAQPLTLQVLVAGNPQDRLRYSFVPRPT--PSTPRPTPDWL 818
Db 802 SGSSAALERIRSFSPLEKPTIQLVMVGHALRPKIYTFMCKKTEFFNAITPFEW 859

RESULT 10
Q68EJ2 PRELIMINARY; PRT; 967 AA.
AC Q68EJ2
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE A disintegrin and metalloproteinase with thrombospondin motifs 1.
GN Name=Adamtsl;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_taxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RC PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shen C.M., Schuller G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RC Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC080237, AAH0237.1; -
DR GO, GO:0007229, P.integrin-mediated signaling pathway; IEA.
DR InterPro: IPR006586; ADAM cysteine.
DR InterPro: IPR010294; ADAM spacer1.
DR InterPro: IPR001590; Peptidase M12B.
DR InterPro: IPR002870; Peptidase M12B_N.
DR InterPro: IPR006025; Pept M_Zn_BS.
DR InterPro: IPR000884; TSP1.
DR InterPro: IPR008085; TSP1.
DR Pfam, PF05986; ADAM spacer1; 1.
DR Pfam, PF01562; Pep M12B_propep; 1.
DR Pfam, PF01421; Reprolysin; 1.

Pfam; PF00090; TSP_1; 3.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SMO0608; ACR; 1.
DR SMART; SMO0209; TSP1; 3.
DR PROSITE; PS02015; ADAM MEPRO; 1.
DR PROSITE; PS0092; TSP1; 3.
DR PROSITE; PS00143; ZINC_PROTEASE; UNKNOWN_1.
KW Integrin.
SQ SEQUENCE 967 AA; 105647 MW; C6349BD8CBFEA24 CRC64;

Query Match 47.3%; Score 2160.5; DB 2; Length 967;
Best Local Similarity 49.5%; Pred. No. 1.1e-130;
Matches 415; Conservative 137; Mismatches 217; Indels 69; Gaps 16;

QY 37 LLLLLL--LLPBARLA--SPLPREBEIVPEPKLNGSVLPKSGAPARLLCLRLQAFQETL 92
Db 35 MLLLLLASITMLLCVRGAHGRTBEDBELVLP-----SLERARGHGSTLLRLDAFGQOL 89
QY 93 LLELEODSGVQVEGLTVQYLQQAPELLGGAF-----PGTYLTGTTINGDPEVSANSL 142
Db 90 HLKLPDSGFLAPGFTLTQVGRSP-----GSEAQHLDPGDLAHCFYSGTVNGDPESSAAL 145
QY 143 HWDGALLGLVQYRGAELHLP-----LEGTP--NSAGGPGAHILRRKSPASGQGP 192
Db 146 SLCEG-VRGAFYLOGEEFFIQAPAVATERLVPAEPKEESTAPFRPHILRRRRSG-GA 203
QY 193 MCNV-----KAPLGSPSP-----RPR-----RAKRFASLRFVETL 223
Db 204 KCGVNDERTLPTSNGRESQNTPDQWFLRNPFGQAGKTPGSGIRKRFVSSPRYVETM 263
QY 224 VVADDKMAAFHAGLKYLLTMAAAKAPKHPSTRNPVSLVTVLVLGSGEPOVGP 283
Db 264 LVADQSMADFHGSLGLKYLTLFSAARFYKHPSTRNSISLVVVKILYIEQKGPVTS 323
QY 284 SAAQTLRSCAWORGLNTPEDSDPHEDTALTFTQDLGCVSTCDTLGMDVGTVCDPAR 343
Db 324 NAALTLENFCSWOKHNSPSDRDPHYDTALTFTQDLGCVSTCDTLGMDVGTVCDPAR 383
QY 344 SCAIVEDDGLQSAFTAHELGHVFNHLDHNSKPCISLNGPLSTSRHVMVPAHVDPEP 403
Db 384 SCSEIVEDDGLQAAFTTAHELGHVFNHLDHNSKPCISLNGPLSTSRHVMVPAHVDPEP 442
QY 404 WSPCSARFTDLDNGYGHCLDKPEALHLPVTPFGKDYDADROCOLTFGDPDRHCPQL 463
Db 443 WSPCSAYMTVSFLDNGHGECLMDKPNPILKPSDLLEPTLYDANRQCOFTFGEESTHCPDA 502
QY 464 PPCCAALWCSHGLNHAMCQTKHSPWADGTPCGPAQACMGRCCLHMDQLQDNFNPAGGW 523
Db 503 ASTCTSLNCTGTSGLLVQCTKHFPWADGTSCEGKVCVSKCNKTKDKHFKATPVHGSW 562
QY 524 GPWPGWDCSRTCGGQVQYTMRECDNPVKNGKYCEGKRVYRSCNIEDCPDNNKTFR 583
Db 563 GPWPGWDCSRTCGGQVQYTMRECDNPVKNGKYCEGKRVYRSCNIEDCPDNNKTFR 622
QY 584 EQCAAYNHRHTLDFKSPGPMWDRYRTGVAPODQCKLTQARALGYVYVLEPRVVDGTP 643
Db 623 EQCEAHNEFSKASFGNEPTVETWTPKYAGVSPKDRCKLTCEAKGIGYFVLQPKVVDGTP 682
QY 644 CSPDSSVVCQRCIHAGCDRIIGSKKFKDKCMVCGDGGSGSKSGSPFRKFRYGNVNV 703
Db 683 CSPDSTSVCCVQGVKAGCDRIIDSKKFKDKCGVCGGSGSTCKLSGTVSTRPGVHDIV 742
QY 704 TIPAGATHILVROQGNPHRS--IYLALKLPDGSYALNGEYTIMSPDTPVLPGAVSLRY 761
Db 743 TIPAGATNIEVKHNRPNRSGNNGSFLAIRAADGTYLNGNFTLSTLEQDLTYKGTV-LRY 801
QY 762 SGATASETLSGHGFLAQPLTLQVLVAGNPQDRLRYSFVPRPT--PSTPRPTPDWL 818
Db 802 SGSSAALERIRSFSPLEKPTIQLVMVGHALRPKIYTFMCKKTEFFNAITPFEW 859

RESULT 11
ATSL_MOUSE

ID ATSI_MOUSE STANDARD; PRT; 968 AA.
 AC P97857; 054768;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE ADAMTS-1 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase
 DE with thrombospondin motifs 1) (ADAM-TS 1) (ADAM-TS1).
 GN Name=Adamts1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RX MEDLINE=98110583; PubMed=9441751; DOI=10.1006/geno.1997.5064;
 RA Kuno K., Lizaasa H., Ohno S., Matsushima K.;
 RT "The exon/intron organization and chromosomal mapping of the mouse
 RT ADAMTS-1 gene encoding an ADAM family protein with TSP motifs.";
 RL Genomics 46:466-471(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97150761; PubMed=8995297; DOI=10.1074/jbc.272.1.556;
 RA Kuno K., Kanada N., Nakashima E., Fujiki F., Ichimura F.,
 RA Matsushima K.;
 RT "Molecular cloning of a gene encoding a new type of metalloproteinase-
 RT disintegrin family protein with thrombospondin motifs as an
 RT inflammation associated gene.";
 RL J. Biol. Chem. 272:556-562(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Limb, and Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feigold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Hopkins R.F., Jordan H., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Diatchenko L., Marusina K., Fawcett A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP CHARACTERIZATION, AND MUTAGENESIS OF GLU-403.
 RX MEDLINE=99303657; PubMed=10373500; DOI=10.1074/jbc.274.26.18821;
 RA Kuno K., Terashima Y., Matsushima K.;
 RT "ADAMTS-1 is an active metalloproteinase associated with the
 RT extracellular matrix.";
 RL J. Biol. Chem. 274:18821-18826(1999).
 RN [5]
 RP FUNCTION.
 RX MEDLINE=20389568; PubMed=10930576; DOI=10.1016/S0014-5793(00)01854-8;
 RA Kuno K., Okada Y., Kawashima H., Nakamura H., Miyasaka M., Ohno H.,
 RA Matsushima K.;
 RT "ADAMTS-1 cleaves a cartilage proteoglycan, aggrecan.";
 RL FEBS Lett. 478:241-245(2000).
 RN [6]
 RP FUNCTION, AND INDUCTION.
 RX MEDLINE=20243757; PubMed=10781075; DOI=10.1073/pnas.080073497;
 RA Robker R.L., Russell D.L., Espey L.L., Lydon J.P., O'Malley B.W.,
 RA Richards J.S.;
 RT "Progesterone-regulated genes in the ovulation process: ADAMTS-1 and

RT cathepsin L proteases.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:4689-4694(2000).
 CC -!- FUNCTION: Cleaves aggrecan, a cartilage proteoglycan, and may be
 CC involved in its turnover. Has angiogenic inhibitor activity (By
 CC similarity). Active metalloproteinase, which may be associated with
 CC various inflammatory processes as well as development of cancer
 CC cachexia. May play a critical role in follicular rupture (By
 CC similarity).
 CC -!- CATALYTIC ACTIVITY: Cleaves aggrecan at the 1691-Glu-I-Leu-1692
 CC site, within the chondroitin sulfate attachment domain.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
 CC matrix.
 CC -!- INDUCTION: Induced in vitro in colon adenocarcinoma cells by
 CC interleukin-1, or in vivo in kidney and heart by
 CC lipopolysaccharide. Also induced by LH stimulation in granulosa
 CC cells of preovulatory follicles.
 CC -!- DOMAIN: The spacer domain and the TSP type-1 domains are important
 CC for a tight interaction with the extracellular matrix.
 CC -!- PTM: The precursor is cleaved by a furin endopeptidase.
 CC -!- SIMILARITY: Belongs to the peptidase M12B family.
 CC -!- SIMILARITY: Contains 1 disintegrin-like domain.
 CC -!- SIMILARITY: Contains 3 TSP type-1 domains.
 CC -!- CAUTION: Ref.2 sequence differs from that shown due to a
 CC frameshift in position 7.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See [http://www.ebi.ac.uk/announcements/](http://www.ebi.ac.uk/announcements)
 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL; AB001735; BAA24501.1; ALT INIT.
 CC EMBL; D67076; BAA11088.1; ALT_FRAME.
 CC EMBL; BC040382; AAH40382.1; -.
 CC EMBL; BC050834; AAH50834.1; -.
 CC HSSP; P07996; 1LSL.
 CC MEROPS; M12.222; -.
 CC MGD; MGI:109249; Adants1.
 CC InterPro; IPR010294; ADAM_spacer1.
 CC InterPro; IPR001762; Disintegrin.
 CC InterPro; IPR006025; Pept_M_Zn_BS.
 CC InterPro; IPR001590; Peptidase_M12B.
 CC InterPro; IPR002870; Peptidase_M12B_N.
 CC InterPro; IPR000884; TSP1.
 CC InterPro; IPR008085; TSP_1.
 CC Pfam; PF05986; ADAM_spacer1.1.
 CC Pfam; PF01562; Pep_M12B_propep; 1.
 CC Pfam; PF01421; Reprolysin; 1.
 CC Pfam; PF00090; TSP_1; 3.
 CC PRINTS; PR01705; TSP1REPEAT.
 CC PROSITE; PS50215; ADAM_MEPRO; 1.
 CC PROSITE; PS50427; DISINTEGRIN_1; FALSE_NEG.
 CC PROSITE; PS50214; DISINTEGRIN_2; FALSE_NEG.
 CC PROSITE; PS50092; TSP1; 3.
 CC PROSITE; PS00142; ZINC_PROTEASE; 1.
 CC Extracellular matrix; Glycoprotein; Heparin-binding; Hydrolase;
 CC Metalloproteinase; Repeat; Signal; Zinc; Zymogen.
 CC SIGNAL 1 48
 CC Potential.
 CC FT PROPEP 49 253
 CC FT CHAIN 254 968
 CC FT DOMAIN 254 476
 CC FT DOMAIN 477 559
 CC FT DOMAIN 560 615
 CC FT DOMAIN 618 725
 CC FT DOMAIN 726 850
 CC FT DOMAIN 855 911
 CC FT DOMAIN 912 968
 CC FT DOMAIN 195 199
 CC FT SITE 206 206
 CC FT METAL 402 402
 CC ADAMTS-1.
 CC Metalloproteinase.
 CC Disintegrin-like.
 CC TSP type-1 1.
 CC Cys-rich.
 CC Spacer.
 CC TSP type-1 2.
 CC TSP type-1 3.
 CC Poly-Arg.
 CC Cysteine switch (Potential).
 CC Zinc (catalytic) (By similarity).

FT	ACT_SITE	403	403	Zinc (catalytic) (By similarity).
FT	METAL	406	406	Zinc (catalytic) (By similarity).
FT	METAL	412	412	Zinc (catalytic) (By similarity).
FT	CARBOHYD	548	548	N-linked (GlcNAc) (Potential).
FT	CARBOHYD	721	721	N-linked (GlcNAc) (Potential).
FT	CARBOHYD	765	765	N-linked (GlcNAc) (Potential).
FT	CARBOHYD	783	783	N-linked (GlcNAc) (Potential).
FT	CARBOHYD	945	945	N-linked (GlcNAc) (Potential).
FT	MUTAGEN	403	403	E->Q: Loss of activity.
FT	CONFLICT	335	335	N -> S (in Ref. 2).
FT	CONFLICT	425	425	T -> S (in Ref. 2).
SQ	SEQUENCE	968 AA	968 AA	425BDA55499FB6C1 CRC64;
Query Match				
Best Local Similarity 49.4%; Pred. No. 1.7e-130;				
Matches 414; Conservative 135; Mismatches 221; Indels 68; Gaps 16;				
QY	37	LLLLLLAS--LLPSARLA--SPLPREBEEIVPEKLVGSLVPSGAPARLLCLOAFGETL	92	
DB	35	MLLLLLASITMLLCARGAHRTEDEELVPLSLERA---PGHDSITTRL-RLDAPGQOL	90	
QY	93	LLELEQDSGVQVGLTVQVQLGOAPPELLGGAE-----PGTYLTGTINGDPESVASL	142	
DB	91	HLKLQPSGFLAFGLTQTVGRSP-----GSEAHLDTGDLAHCFFYGVNGDPGSAAL	146	
QY	143	HWDCGALLGVLOVGAELHLQPLEG-----GTP--NSAGPGGAHLIRKSPASGQGP	192	
DB	147	SLCEG-VRGAFYLGQEBFFIOPAPGVATERLAPVPEESSARPQPHILLRRRSGG-GA	204	
QY	193	MCNV-----KAPLGSPSRPR-----RAKRFASLSRFVETL	223	
DB	205	KCGVMDDETLPSTDSRPESQNTNRQWVPDTPQDAGKPGSGIRKRVFSFVETM	264	
QY	224	VVADKMAAFHAGLKYLLTWMAAAKAFKPSIRNPVSLVTVRLVGLSGEGPQVGP	283	
DB	265	LVAQSWADFGSLGKHYLLTLFVAARFYKPSIRNSISLVVVKILVIEEQGPEVTS	324	
QY	284	SAATLRSFCWAGRLNTPEDDPDFTALLFRQDLQGVSTCDTGMADVGTVCDDPAR	343	
DB	325	NAALTNRNFCWQKHSNPSRDEPHYDTALLFRQDLQGVSTCDTGMADVGTVCDDPSR	384	
QY	344	SCAIVDDGLQSAFTAAHELGHVNFMLHNSKPCISLNGPLSTSRHVMAFVMAHVPDEP	403	
DB	385	SCSVIEDGLQAFATTAHELGHVNFMPHDDAKHCSLNGVTGDS-HLWASMLSLDHSQP	443	
QY	404	WSPCSARFITDLNGYGHCLLDKPEAPLHLPVTFPGKYDADQCQTLFGPDSRHCPQL	463	
DB	444	WSPCSAYVWTSFLDNGHGECLMDKPNBPKLPSDLPLGTLYDANRQCOFTFGESKHCPDA	503	
QY	464	PPCAALWCSHLNGHAMCOTKHSWADGTPCGPAQACMGGRCLHMDLOQDFNIPQAGGW	523	
DB	504	ASTCTTLTCTGTSGLLVCQTQKHPWADGTCGEGKWCVSGKCNKTKDKHFAFVHGSW	563	
QY	524	GPWGPWGDSCRTCGGGVQFSSRDCTRPVPRNGKYCEGRTRFRSCNTEDCPTGSALTFR	583	
DB	564	GPWGPWGDSCRTCGGGVQYTWEECDNPVFKNGKYCEGRVRYRSCNTECDPNNKGTFR	623	
QY	584	EQQCAAYNRHRLDFKSPFGPMWVRYTGVAPDQCKLTCCARALGVYVLEPRVVDGTP	643	
DB	624	EQQCAAHNEFSKASFGNEPTWPTKYAGVSPKDRCKLTCEANGIGYFVLPQKVVDTGP	683	
QY	644	CSPDSSVCQGRCHTAGCDRIIGSKKFKDKMVCVGGGSGKSGKSGFRKFRFYGNVNV	703	
DB	684	CSPDSTSVCCQGVKAGCDRIIDSKKFKDKGVCVGGSGTCKKWSGIVTSTRPGYHDIV	743	
QY	704	TIPAGATHILVRQGNFGRHS--IYALKLPDGSVALNGEYTLMPSTDTVLPGVSLRY	761	
DB	744	TIPAGATNIEVXHRNQGRNNGSFLAIRAADGTVILNGNFTLSTLEODLTYKGTV-LRY	802	
QY	762	SGATASETLSHGFLAQLTLQVLVAGNPQDTRLRYSFVPRTPS-TPRTPDQWL	818	
DB	803	SGSSAALIRSPSPLEKPTIQLVMVGHALRPKIKFTYFMKKTKTESFNALITFSEW	860	

RESULT 12	ATSI HUMAN	STANDARD;	PRT;	967 AA.
ID	Q9UHI8; Q9NSJ8; Q9P2K0; Q9U8H3; Q9UP80;			
AC	30-MAY-2000 (Rel. 39, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	ADAMTS-1 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase)			
DE	with thrombospondin motifs 1) (ADAM-TS 1) (ADAM-TS1) (METH-1).			
GN	Name=ADAMTS1; Synonyms=KIAA1346, METH1;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Casas C., Pritchard M.A., Estivill X., Arbones M.L.;			
RT	"Cloning, characterization and mapping on human chromosome 21 of the			
RT	orthologue of murine Adamts-1.;"			
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A., AND FUNCTION.			
RC	TISSUE=Heart;			
RX	MEDLINE=99367466; PubMed=10438512; DOI=10.1074/jbc.274.33.23349;			
RA	Vazquez F., Hastings G., Ortega M.-A., Lane T.F., Oikemus S.,			
RA	Lombardo M., Iruela-Arispe M.L.;			
RT	"METH-1, a human orthologue of ADAMTS-1, and METH-2 are members of a new			
RT	family of proteins with angio-inhibitory activity.;"			
RL	J. Biol. Chem. 274:23349-23357(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Endothelial cells;			
RX	MEDLINE=20247184; PubMed=10785405;			
RA	Glienke J., Schmitt A.O., Pillarsky C., Hinzmann B., Weiss B.,			
RA	Rosenthal A., Thierach K.H.;			
RT	"Differential gene expression by endothelial cells in distinct			
RT	angiogenic states.;"			
RL	Eur. J. Biochem. 267:2820-2830(2000).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=20181126; PubMed=10718198;			
RA	Nagase T., Kikuno R., Ishikawa K.-I., Hirose M., Ohara O.;			
RT	"Prediction of the coding sequences of unidentified human genes. XVI.			
RT	The complete sequences of 150 new cDNA clones from brain which code			
RT	for large proteins in vitro.;"			
RL	DNA Res. 7:65-73(2000).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=20289799; PubMed=10830953; DOI=10.1038/35012518;			
RA	Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,			
RA	Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,			
RA	Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,			
RA	Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,			
RA	Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,			
RA	Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,			
RA	Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,			
RA	Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,			
RA	Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,			
RA	Ranger J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,			
RA	Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,			
RA	Lehrach H., Reinhardt R., Yaspo M.-L.;			
RT	"The DNA sequence of human chromosome 21.;"			
RL	Nature 405:311-319(2000).			
RN	[6]			
RP	SEQUENCE OF 418-967 FROM N.A.			
RC	TISSUE=Melanoma;			
RA	Blum H., Bauresachs S., Mewes H.-W., Weil B., Wiemann S.;			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
CC	!- FUNCTION: Cleaves aggrecan, a cartilage proteoglycan, and may be			
CC	involved in its turnover (By similarity). Has angiogenic inhibitor			
CC	activity. Active metalloprotease, which may be associated with			

various inflammatory processes as well as development of cancer cachexia. May play a critical role in follicular rupture.

-1- CATALYTIC ACTIVITY: Cleaves aggrecan at the 1938-Glu-Leu-1939 site, within the chondroitin sulfate attachment domain.

-1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).

-1- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).

-1- DOMAIN: The spacer domain and the TSP type-1 domains are important for a tight interaction with the extracellular matrix.

-1- PTM: The precursor is cleaved by a furin endopeptidase (By similarity).

-1- SIMILARITY: Belongs to the peptidase M12B family.

-1- SIMILARITY: Contains 1 disintegrin-like domain.

-1- SIMILARITY: Contains 3 TSP type-1 domains.

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EMBL: AF170084; AAF15317.1; -; ALT_INIT.

EMBL: AF060152; AAD48080.1; -; ALT_INIT.

EMBL: AF207664; AAF23772.1; -; ALT_INIT.

EMBL: AB037767; BAA92584.1; -; ALT_INIT.

EMBL: AP001697; BAA95502.1; -; ALT_INIT.

EMBL: AL162080; CAB82413.1; -; ALT_INIT.

PIR: T47158; T47158.

HSSP: P07996; 1LSL.

MEROPS: M12.222; -.

Genew: HGNC:217; ADAMTS1.

H-InvDB: HIX0016042; -.

MIM: 605174; -.

GO: GO:0008337; F:metallopeptidase activity; TAS.

GO: GO:0007229; P:integrin-mediated signaling pathway; TAS.

GO: GO:0008285; P:negative regulation of cell proliferation; TAS.

InterPro: IPR006586; ADAM cysteine.

InterPro: IPR010294; ADAM_spacer1.

InterPro: IPR001762; Disintegrin.

InterPro: IPR001590; Peptidase M12B.

InterPro: IPR002870; Peptidase M12B_N.

InterPro: IPR006025; Pept M_Zn_BS.

InterPro: IPR000884; TSP1.

InterPro: IPR008085; TSP1.

Pfam: PF05986; ADAM_spacer1; 1.

Pfam: PF01562; Pep_M12B_propep; 1.

Pfam: PF01421; Reprolysin; 1.

Pfam: PF00090; TSP 1; 3.

PRINTS: PR01705; TSP1REPEAT.

SMART: SM00508; ACR; 1.

SMART: SM00209; TSP1; 3.

PROSITE: PS02015; ADAM_MEPRO; 1.

PROSITE: PS00427; DISINTEGRIN 1; FALSE_NEG.

PROSITE: PS02014; DISINTEGRIN 2; FALSE_NEG.

PROSITE: PS00092; TSP1; 3.

PROSITE: PS00142; ZINC_PROTEASE; 1.

Extracellular matrix; Glycoprotein; Heparin-binding; Hydrolase;

Metalloprotease; Repeat; Signal; Zinc; Zymogen.

POTENTIAL

FT SIGNAL 1 49

FT CHAIN 50 252

FT CHAIN 253 967

FT CHAIN 253 475

FT DOMAIN 476 559

FT DOMAIN 559 614

FT DOMAIN 617 724

FT DOMAIN 725 849

FT DOMAIN 854 905

FT DOMAIN 908 967

FT DOMAIN 988 1011

FT SITE 198 198

FT SITE 401 401

FT METAL

By similarity.

ADAMTS-1

Metalloprotease.

Disintegrin-like.

TSP type-1 1.

Cys-rich.

Spacer.

TSP type-1 2.

TSP type-1 3.

Poly-Lys.

Cysteine switch (Potential).

Zinc (catalytic) (By similarity).

FT	ACT SITE	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900	901	902	903	904	905	906	907	908	909	910	911	912	913	914	915	916	917	918	919	920	921	922	923	924	925	926	927	928	929	930	931	932	933	934	935	936	937	938	939	940	941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960	961	962	963	964	965	966	967	968	969	970	971	972	973	974	975	976	977	978	979	980	981	982	983	984	985	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000
FT	METAL	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900	901	902	903	904	905	906	907	908	909	910	911	912	913	914	915	916	917	918	919	920	921	922	923	924	925	926	927	928	929	930	931	932	933	934	935	936	937	938	939	940	941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960	961	962	963	964	965	966	967																																	

Q8NE26 Q8NE26 PRELIMINARY; PRT; 967 AA.

AC Q8NE26; (1)

DT 01-OCT-2002 (Tremblrel. 22, Created)

DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)

DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

DE A disintegrin and metalloprotease with thrombospondin motifs-1, preproproteasin.

DE DE Name=ADAMTS1.

GN Name=ADAMTS1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RN SEQUENCE FROM N.A.

RP TISSUE=Testis;

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.K., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Testis;

RA Director MGC Project;

RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

DR HBSL; BC036515; AHA36515.1; -.

DR HBSL; P07996; 1L5L.

DR GO; GO:0004223; P:metalloendopeptidase activity; IEA.

DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPRO00586; ADAM cysteine.

DR InterPro; IPRO10294; ADAM spacer1.

DR InterPro; IPRO01128; Cytochrome P450.

DR InterPro; IPRO01590; Peptidase M12B.

DR InterPro; IPRO02870; Peptidase M12B_N.

DR InterPro; IPRO06025; Pept M_Zn_BS.

DR InterPro; IPRO00884; TSP1.

DR InterPro; IPRO00805; TSP1.

DR Pfam; PF05986; ADAM spacer1; 1.

DR Pfam; PF01562; Pep_M12B_propep; 1.

DR Pfam; PF01421; Reprolysin; 1.

DR Pfam; PF00090; TSP 1; 3.

DR PRINTS; PR01705; TSP1REPEAT.

DR SMART; SM00209; ACR; 1.

DR PROSITE; PS02115; ADAM_MEPPO; 1.

DR PROSITE; PS00866; CYTOCHROME_P450; UNKNOWN_1.

DR PROSITE; PS00992; TSP1; 3.

DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.

DR Integrin; Metalloprotease; Protease.

SK SEQUENCE 967 AA; 105387 MW; PFID399674201C3D CRC64;

Query Match. 46.5%; Score 2127; DB 2; Length 967;

Best Local Similarity 49.4%; Pred. No. 1.6e-128;

Matches 414; Conservative 127; Mismatches 227; Indels 70; Gaps 18;

Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF541975; AAN17331.1; -.
DR HSSP; P07996; 1LSL.
DR MEROPS; M12.222; -.
DR GO; GO:0004222; F-metalloendopeptidase activity; IEA.
DR GO; GO:0005508; Proteolysis and peptidolysis; IEA.
DR InterPro; IPR006586; ADAM cysteine.
DR InterPro; IPR010294; ADAM spacer1.
DR InterPro; IPR001590; Peptidase M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR Pfam; PF00090; TSP 1; 3.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00608; ACE; 1.
DR SMART; SM00209; TSP1; 3.
DR PROSITE; PS00215; ADAM_MEPRO; 1.
DR PROSITE; PS00092; TSP1; 3.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 759 AA; 83409 MW; C1854C048918C8E9 CRC64;

Query Match 43.7%; Score 1998.5; DB 2; Length 759;
Best Local Similarity 53.5%; Pred. No. 2.4e-120;
Matches 361; Conservative 113; Mismatches 158; Indels 43; Gaps 10;

QY 156 RGAEHLPLEGQT-----PNSAGGCAHLTRKSPASGQPMCNVYKAPLGSFSPRP 207
DB 8 RGAEPPGQ--DAGTQWAPDRAPQARGP-----TGTSI----- 40

QY 208 RRAKRPASLRFVETLVVADKKMAAFHAGLKRYLLTVMAAAKAFKPSIRNPVSLVVT 267
DB 41 -RKRFVSPRYVETMLVADQNAEFHSGLKHYLLTFSVAARLYKPSIRNSVSLVV 99

QY 268 RLVLGSGEGPQVPSAAGTLRSFCAWQGLNTPEDSDPHDPTAILFTRODLGVSTC 327
DB 100 KILVYEEQKGPVTSNAALTANFCNQKHNPSPSDRAEYDVTAILFTRODLGCAQC 159

QY 328 DTGLGADVTCVPARSCAIVEDDGLQSAFTAAHELGHPVFMHLDNSKCSISLNGPLSTS 387
DB 160 DTGLGADVTCIPSPSCSVIEDDGLQAAFTTAHELGHPVFMHDPHDAKQCASING-VNRD 218

QY 388 RHVMPVMAHVDEEPSPSCSAFIITDFLDNGYGHCLDKPEAPLHLPTVFPCKDYDADR 447
DB 219 SHWMAWMLNDRSQWSPSCSAFYITSLDNGHGECLMDKQSPQIQPSDLPTLLDADR 278

QY 448 QCQLTFGPDNRHCPQLPPPCAAALWCSEHLNGHAMCQTKHSPWADGTPCGPAQACMGGRCL 507
DB 279 QCQTFGEESKHCPDAASTCTLLWCTGTSGLLVLCQTKHFPWADGTSCEGRWCNVGKCV 338

QY 508 HMDQLQDFNI PQAGHGPGWPGWDCSRTCGGVQFSSRDCTRPVNGKYCEGRTRFR 567
DB 339 NKTDRKHFTPVHSGWPGWPGWDCSRTCGGVQVYTRBECNDVPVKNKGKCYCEGRVYR 398

QY 568 SCNTECPGTSALTFREEOCAAYNHRIDL-FKSPGPMWVPRYTGVAPQDOCKLTCQAR 626
DB 399 SCNIECPDNGKTFREEOCAHNEFSKASFGSGPA-VEWTPKAVGSPKDRCKLLCQAK 457

QY 627 ALGYVYLPRVVDGTPCGSPDSSVCVQGRICIHAGCDRIIGSKKFKDKMVCGGDGGCS 686
DB 458 GIGYFVFLQPKVVDGTPCGSPDSTSVCVQGVKAGCDRIIDSKKFKDKGICGGNGSTCK 517

QY 687 KQSGSFRKFRYGNVVTIPAGATHILVROQGNPHRS--IYLAKLPDGSYALNGEYTL 744
DB 518 KISGVSYSKAPGVHDVITPTGATNTEVKQNRGSRNNGSFIAAADGTYLNGDFTL 577

QY 745 MPSPDVLVPGAVSLYSGATASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFVFR 804
DB 578 STLEQDITYKGSV-LYISGSSALERIRFSPLKEPLTLQVLTVGNALRPKITYITFVK 636

QY 805 PTPS-TPRPTQDWL 818

DB 637 KKESFNAIPTFSEWV 651
RESULT 15
AT15_HUMAN STANDARD; PRT; 950 AA.
ID AC Q8TB58;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE ADAMTS-15 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase
DE with thrombospondin motifs 15) (ADAM-TS 15) (ADAM-TS15).
GN Name=ADAMTS15;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=21856482; PubMed=11867212; DOI=10.1016/S0378-1119(01)00861-7;
RX Cal S., Obaya A.J., Llamazares M., Garabaya C., Quesada V.,
RA Lopez-Otin C.;
RT "Cloning, expression analysis, and structural characterization of
RT seven novel human ADAMTSs, a family of metalloproteinases with
RT disintegrin and thrombospondin-1 domains.";
RL Gene 283:49-62(2002).
CC -!- COPACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
CC matrix (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed in fetal liver and kidney, but not
CC in any of the adult tissues examined.
CC -!- DOMAIN: The spacer domain and the TSP type-1 domains are important
CC for a tight interaction with the extracellular matrix (By
CC similarity).
CC -!- PTM: The precursor is cleaved by a furin endopeptidase (By
CC similarity).
CC -!- SIMILARITY: Belongs to the peptidase M12B family.
CC -!- SIMILARITY: Contains 1 disintegrin-like domain.
CC -!- SIMILARITY: Contains 3 TSP type-1 domains.

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CC EMBL; AJ315733; CAC86014.1; -.
DR HSSP; P07996; 1LSL.
DR MEROPS; M12.025; -.
DR Genew; HGNC:16305; ADAMTS15.
DR MIM; 607509; -.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR001590; Peptidase M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR Pfam; PF00090; TSP_1; 3.
DR SMART; SM00209; TSP1; 3.
DR PROSITE; PS00215; ADAM_MEPRO; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; FALSE_NEG.
DR PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
DR PROSITE; PS00214; DISINTEGRIN_2; FALSE_NEG.
DR PROSITE; PS00092; TSP1; 3.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Extracellular matrix; Glycoprotein; Hydrolase; Metalloprotease;

Qy 716 QQNGPG--HRSIYIALKLPDGSYALNGEYTLMPSTDDVVLPGAVSLRYSGATAASETLSG 773
Db 713 QRGYKGLIGDDNYLALKNSOGKYLINGHFVVSAVERDLVVKGL-LRYSGTGTAVESLQA 771
Qy 774 HGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPTSTPRTPQD 816
Db 772 SRFILEPLTVEVLVSGKWTTPRVYSFYLKPEPREDKSSHPKD 814

Search completed: April 1, 2005, 12:51:40
Job time : 192 secs

KW Repeat; Signal; Zinc; Zymogen.
FT SIGNAL 1 17 Potential.
FT PROPEP 18 212 By similarity.
FT CHAIN 213 950 ADAMS-15.
FT DOMAIN 213 427 Metalloprotease.
FT DOMAIN 428 515 Disintegrin-like.
FT DOMAIN 516 571 TSP type-1 1.
FT DOMAIN 572 700 Cys-rich.
FT DOMAIN 701 838 Spacer.
FT DOMAIN 839 895 TSP type-1 2.
FT DOMAIN 896 949 TSP type-1 3.
FT SITE 174 174 Cysteine switch (Potential).
FT METAL 361 361 Zinc (catalytic) (By similarity).
FT ACT SITE 362 362 By similarity.
FT METAL 371 371 Zinc (catalytic) (By similarity).
FT METAL 371 371 Zinc (catalytic) (By similarity).
FT CARBOHYD 141 141 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 591 591 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 623 623 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 679 679 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 950 AA; 103286 MW; 5DFBE18285CCCC3B CRC64;

Query Match 41.9%; Score 1915; DB 1; Length 950;
Best Local Similarity 46.3%; Pred. No. 7.4e-115; Indels 52; Gaps 16;
Matches 381; Conservative 123; Mismatches 267;

Qy 37 LLLILLASLPARLSPREBEIVPEKINGSVL-----PGSGAPARLLCRLOAF 88
Db 1 MLLGIILTAPAGTAGGSEPEREVVPIRLDPDINGRRYVWRGPDSDGQGLIFQITAF 60
Qy 89 GETLLLEQDSGVQVGLTVQYLGQAPL-LLGGAEP--GTYLTGTNGDPESVASLHWD 145
Db 61 QEDFYLLHTLTPAOPAFAPAFSTHGLVPLQGLTGGSDLRRCFYSGDVNAEPDFAAVSLC 120
Qy 146 GGALGLVQLVGEALHLPLEGGTPNSA--GGCAHILRRK---SPASQGGPMCNV--- 196
Db 121 GG-LRGAFYRGAEYVISPLENASAPAAQRNSQAHLLQRRGVPGGPGDPTSRGCVASG 179
Qy 197 -----KAPLGSPPRPR--RAKRFASLSRFVETLVVADDDKMAAFHGAGLK 239
Db 180 WNPAILRALDPYKPRRAGFGESRRRRSGRAKRFVSIPIRYVETLVVADESNNVFKPHGADLE 239
Qy 240 RYLLTVMAAAKAFKHPISIRNPVSLVTRVLVILGSEEGPOGPSAAQTLSRFCAMQRL 299
Db 240 HYLTLTATAARLYRHPILNIPINIVVVKVLLLRDRSGPKVTGNALTLENFCWQKLL 299
Qy 300 NTPEDSDPDHFDTAILFTRODLGVSTCDTTLGMADVGTVCDDPARSCAIVEDDGLQSAFTA 359
Db 300 NKVSKHPEYWDTAILFTRODLGVSTCDTTLGMADVGTVCDDPARSCAIVEDDGLQSAFTA 359
Qy 360 AHELGHVFNMLHDSKPCISLNGPLTSRHYWAPVMAHVDPPEPWPSCSARFITDFLDNG 419
Db 360 AHELGHVFNMLHDSKPCISLNGPLTSRHYWAPVMAHVDPPEPWPSCSARFITDFLDNG 419
Qy 420 YGHCLLDKPEAPLHPVTPFGKDYDADRCQQLTFGDSRHCPQLPFPCCALWCSEHLNGH 479
Db 419 HGCCLLDQPSKFIISLPEDLPAGSYLSQCELAFGVSGKPCPYM-QYCTKLWCTGKAKGQ 477
Qy 480 AMCQTKHSPWADGTPCGPAQACMGRCCLHMDQLDFNIPQAGGPGWPGWDCSRTCCGG 539
Db 478 MVCQTRHFPWADGTSCEGKCLKGCACVERHNLNKHRYD--GSWAKNDPYGPCSRTCCGG 535
Qy 540 VQFSSRDCTRPVRNGGKYCEGRRTRFRSCNTDCP-TGSALTFRREQCAA---YNHRTD 595
Db 536 VQLARRQCTNPTFANGGKYCEGVVRKYRSCNLEPCFPSSASGKSFREEOCEAFNGYNHSTN 595
Qy 596 LFKSFPFGMDWPRYTGVAPOCKLTCQARALGYVYVLEPRVVDGTFCSPDSSSVCVQG 655
Db 596 RLTL---AVAWPKYSGVSPRDKCLICRANGTYGYVLAIPKVDGTLCSPDSTSVCVQG 652
Qy 656 RCHHACDRIIGSKKFKDKMVGCGSGCSKOSGSKFRFRYGNVVTIPAGATHILVR 715
Db 653 KCIKAGCDGNLGRKRFKCGVCGGDNKSKCKVTGLFTKPMHGYNFVVAIPAGASSIDIR 712